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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1 gaattccacttgatcgcgga.....ccctgagctacgagaagctt 1758
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em_htgo_mus:*
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em_htg_inv: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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98 5 4
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15 16
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c 21
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0 3 3 3 3 3 9 8
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444 544

ALIGNMENTS

RESULT 1		
BD011857		•
LOCUS	BD011857 1758 bp DNA	linear PAT 02-AUG-2002
DEFINITION	Ö	or producing
	D-aminoacylase.	
ACCESSION	BD011857	
VERSION	BD011857.1 GI:22092046	
KEYWORDS	WO 0078926-A/1.	
SOURCE	unidentified.	
ORGANISM	unidentified	
•	unclassified.	
REFERENCE	1 (bases 1 to 1758)	
AUTHORS	Takeuchi, K., Koide, Y., Hirose, Y., Moriguchi, M. and Isobe, K.	chi,M. and Isobe,K.
TITLE	Transformant microorganism and process for producing D-aminoacylase	or producing D-aminoacylase
JOURNAL	Patent: WO 0078926-A 1 28-DEC-2000;	

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PN WO 0079926-A/1

PD 28-DEC-2000

PF 15-JUN-2000 WO

PR 17-JUN-1999 JP

PI KENICHI TAKEUCH

MITSUAKI MORIGUCHI,

PI KIMIYASU ISOBE

PC C12N1/21,C12N15

CC

FH Key
 CCGCTGAGCGCGTGGCGGCATCTACGCCACCCACATGCGCGAAGGCGAAGGCGACACATC 720
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C12N1/21,C12N15/52,C12N9/80
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WO 0078926-A/1
28-DEC-2000
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17-JUN-1999 JP 99P 170555
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RESULT

	1 CTGAGCTACGAGAAGCTT 1758 	y 174 b 174	Db VQ
1740 1740	1 TCGCAGGCCAGCGGCATCGCGGTCTCGACCCTGTCCAAGGCCGAGCTGGGCCAGATCGCC	y 168 b 168	D 03
1680 1680	11 GTGATGGGGGGGGGCGTGGGGGCGGAGGGCGAAAATGACCCTGCAAGACCTG	y 162 b 162	ad Ao
1620 1620	1 CGCTACATGGCCCCTCCCTCCGCTCGCAATACGGCCCCACCCGATATCGTGGGCAAGGAA	y 156 b 156	DF OA
1560 ·	1 CCCTTACAATCCGGCGTGAACGGGGCGGCGTGCCGCCCCTCCCAACCCTGGACGCAAAC	y 150 b 150	Dt. Qy
1500 1500	1 TTCACCGGCCAGCATGCCGGCCGCGCTGCTCGCACGCCCGGCCCCTGAGCCCCGGCGCCAG	y 144 5 144	0y
1440	1 CGCGCCGCCGGCATCCATTCCGTGTACGTCAACGGCGCGCCGGTCTGGCAAGAGCAGGCG	y 138 5 138	4d 60
1380 1380	1 CTGGTGGTGTTCGACCCGGCCACGGTGGCCGATACCGCCACCTTCGAACACCCTACCGAG	132	Db
.1320 1320	1 ACCGCCGCGCGTTCGGCCTGGCCGGGCGGGCAGCTGCAGGCCGGGTACTTCGCCGAC	126 126	dd Qy
1260 1260	1 TATGCGCGCGACCTGGGCCTGTTCCCGCTGGAGACGGCGGTATGGAAGATGACCGGCCTG	7 120 5 120	gg. VQ
1200 1200	1 CCGCACGAGGAGCGCCCGCATCCGCGCCCTGTGGGGCACCTTCCCGCGGGTGCTGGGGCAC	0 114	bb Qy
1140 1140	1 GAACCCGACGTGCAGCGCATCCTGGGGTTCGGCCCGACCATGATCGGCTCCGACGGCCTG	108	dg Qy
1080	1 TCCAAGTACGACGTGGTGCCCGAGCTGCAGCCGGCGGCGCCATCTACTTCATGATGGAC	, 102 5 102	ğ ğ
1020 1020	1 AAGCCCTTCCCCGAACTGAGCGGGCGCGACCTGGATGAAGTCGCGGGCGAGCGCGAAA 	96	qq VQ.
960	1 TCCACCATGCTCAAGCAGGACCGCGTGCTGCTGGCGGGACGCACCATCATCACCTGGTGC	90	da Vo
900	1 ATCGAGGCCGCCATGGCGCCCAGGACGTCTCGCTGGACGCGTATCCCTACGTGGCCGGC	84	74 50
840 840	1 TCGCACCACAAGGTCATGGGCCAGCCCAAFTTCGGCCGCTCGCGGGAGACGCTGCCGCTG	78	Db Qy
780		72	Db

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
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                                                                                                                                                                                                                                              Patent: JP 2001000185-A:1 09-JAN-
AMANO PHARMACEUT CO LTD

OS Alcaligenes xylosoxydans sub
PN JP 2001000185-A:1
PP 09-JAN-2001
PF 17-JUN-1999 JP 1999170555
PR KENICHI TAKEUCHI, YOSHINAO KO
MITSUAKI MORIGUCHI,
PI KIMIYASU ISOBE
PC C12N15/09,C12N1/21,C12N9/80/
PC C12R1:19),
PC C12N15/00,(C12N15/00,C12R1:0
CC
FH Key Location/Qua
FT source 1 1758
FT Source 1 1758
FT
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Takeuchi, K., Koide, Y., Hirose, Y., Moriguchi, M. and Isobe, K.
Transformed microorganism and process for producing D-aminoamylase
Patent: JP 2001000185-A 1 09-JAN-2001;
AMANO PHARWACEUT CO LTD
OS Alcaligenes volcto
PN JP 200100185-A/1
PD 09-JAN-2001
PD 09-JAN-2001
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Location/Qualifiers
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//organism-"unidentified"
//db_xref-"'taxon:32644"
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12N15/09,C12N1/21,C12N9/80//(C12N15/09,C12R1:05),(C12N9/80,
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Pred. No. 9e-183;
Mismatches 0
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Patent number JP03074329-T/1, 12-JAN-2001.
AMANO PHARMACEUTICAL CO LTD.
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                                         GenBank staff at the National Library
entry (NCBI gibbsq 174864) from the or
This sequence comes from Fig. 3.
Location/Qualifiers
                                                                                                     Cloning and sequencing of a gene encoding D-aminoacylase from Alcaligenes xylosoxydans subsp. xylosoxydans A-6 and expression the gene in Escherichia coli
Biosci. Biotechnol. Biochem. 59 (11), 2115-2119 (1995)
                                                                                                                                          Wakeyama, M., Katsuno, Y., Hayashi, S., Woriquchi, M.
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Query Match
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SDAAAHTRVDVSGLVVARGFIDSHTHDDNYLLARRDMTPKISQCVTTVVTGNGGISLA
PLAHANPEPALDLLDEGGSYREERFADYLDALKARTPAAVNDHSTL
RAAMPDALDLLDEGGSYREERFADYLDALKARTPAAVNDHSTL
RAAMRDLABEAMASGAIGISTGAFYPPAARATTEEIIEVCRPLSAHGGIY
ATHMRDEGEHIVAALEETFRIGRELDVPVISHKVMGQPNFGRREFTLPLIBAMAR
DDVSLDAYFYVAGSTMLKQDRVLLAGRTITMGKFPEBLSGRDLDEVARERGKSKYDV
VPELQPAGAIYFMMDEPDVQRILAFGPTMIGSDGLPHDERPHPRLWGTFPRVLGHYAR
DLGLIFPLETAVNKMTGLFAARFGLAGRGQLQAGYFABLVVFDPATVADTATFEHPTER
AAGHSYVNGAPYMGBAFTGQAAGRGLAGRGALVARTAA"

282 t
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partial peptide sequencing; This sequence comes
3; N-acyl-D-amino acid amidohydrolase"
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/protein_id="AAB35881.1"
/db_xref="GI:1488357"
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                                                                               TCGCAGGCCAGCGCATCGCGGTCTCGACCCTGTCCAAGGCCCGAGCTGGGCCAGATCGCC 1740
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Alcaligenes xylosoxidans DNA
amidohydrolase, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (13-FEB-1995) Mamoru Wakayama, Oita University, Applied Chemistry; Dannoharu, Oita, Oita 870-11, Japan (Tel:0975-69-3311(ex.746), Fax:0975-69-7957)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alcaligenes xylosoxydans subsp. xylosoxydans A-6 and expression the gene in Escherichia coli
Biosci. Biotechnol. Biochem. 59 (11), 2115-2119 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning and sequencing of a gene encoding D-aminoacylase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alcaligenes xylosoxydans subsp. xylosoxydans
J. Biochem. 118 (1), 204-209 (1995)
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Saka, K. and Moriguchi, M.
Primary structure of N-acyl-D-glutamate amidohydrolase
Primary structure of N-acyl-D-glutamate amidohydrolase
Primary structure of N-acyl-D-glutamate Amidohydrolase
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N-acyl-D-amino acid
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/product="N-acyl-b-amino acid amidohydrolase"
/product="N-acyl-b-amino acid amidohydrolase"
/protein_id="BAA08349.1"
/db_xref="Gi:1881397"
/db_xref="Gi:1881397"
/db_xref="Gi:VapecfIDSHTHDDNYLLERRDMTPKISGGYTTVYTGNCGISLA
SDAAAHTRYDYSGLYVAPCFIDSHTHDDNYLLERRDMTPKISGGYTTVYTGNCGISLA
FLAHANPPAPLDLIDEGGSYRFERFADYLDALEATPAAVNAACMYGHSTLRAAVMPDL
QRAATDEEIAAMRDLAEEAMASGAIGISTGAFYPPAARATTEEIIEVCRPLSAHGGIY
ATHHRDEGGHIVAALEETFRIGRELDVFVVISHKVMGQPNFGRSREFLPLIEAAMAR
QDYSLDAYFYVAGSTMLKQDRYLLAGRTITTMCKPFPELSGRDLDEVAAERGKSKYDV
VPELQPAGAIYFMADEPDYQRILAFGFMIGSDCLPHDERPHPRLWGTFPRVLGHYAR
DLGLFPLFTAVWKMTGLTAARFGLAGRGQLQAGYFADLVVFDPATVADTATFEHPTER
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DLGLFPLETAVWKMTGLTAAKFGLAERGQVQFGYYADLVVFDPATVADSATFEHPTER
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Score 1088.6;
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Cloning, expression, and nucleotide sequence of the N-acyl-D-aspartate amidohydrolase gene from Alcalige xylosoxydans subsp. xylosoxydans A-6
J. Ferment. Bioeng. 80, 311-317 (1995)
3 (bases 1 to 1497)
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N-acyl-D-amino acid amido
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Direct Submission
Submitted (13-FEB-1995) Mamoru Wakayama, Oita Chemistry; Dannoharu, Oita, Oita 870-11, Japan (Tel:0975-69-3311(ex.746), Fax:0975-69-7957)
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/protein_id="BaA08350.1"
/db_xref="G1:1800111"
/translation="MTDRSTLIDAPAQADFIIAGATLIDGGGGBARQGDLAVRGGRIV
ALGDFAHAPGVPVIDARGLALAPGFIDSHTHDDGYLLAHPEMLPKVSQGITTVVTGNC
GISLAPLSRRQIPQPLDLLGGPELFREATFROWLRALAETPAAVNVIPLVGHTTLRVA
VMDDTGRAATDAERAAMRALLDEALQAGAFGVSTGTFYPPASAAPTDEIIDVCQPLRG
RAGAIYATHLKDEADHIVPAMEEALLIGRELDCRVVESHHKLAGERHHGRSRFTLINI
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LDDEAAIARLAFAGAIYFLMDQADVNRIFSHPLTTVGSDGLFPDPHPHPRQWGTFTNV
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Ralstonia
Bacteria;
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Salanoubat,M., Genin,S., Artiguenave,F., Gouzy,J., Mangenot,S.,
Arlat,M., Billault,A., Brottier,P., Camus,J.C., Cattolico,L.,
Chandler,M., Choisne,N., Claudel-Renard,C., Cunnac,S., Demange,N.,
Gaspin,C., Lavie,M., Moisan,A., Robert,C., Saurin,W., Schiex,T.,
Siguier,P., Thebault,P., Whalen,M., Wincker,P., Levy,M.,
Weissenbach,J. and Boucher,C.A.
Genome sequence of the plant pathogen Ralstonia solanacearum
2 (bases 1 to Boucher, C.A.
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Proteobacteria;
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CDS
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http://sequence.toulouse.inra.fr/R.solanacearum.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INR, URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire INRA, BP27, F31326 Castanet-Tolosan Cedex
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BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene name confidence : hypothetical predicted by Codon_usage predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MADSVQYQQVADVPGLVLSAGRFSQFSFERHFHLDFHVGLVTAG
VQRQRFKGKTVLLGPGCISLMPPGEIHDGVAEGDGAYTLKTFRLSQALLANLAQDISG
TDHEPELAATLLEDPALAGHLLRLHDAMQHSGASTLQVQSEWLALLAFILKQSRALIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predicted by Codon_us
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene name confidence : hypothetical
                                                   /evidence=not_experimental
complement(2462. .3139)
/gene="RSp1117"
                                                                                                                                                                                                                                                                                                                    ADDCTARVEQTLSELFEREVKVFLVPTGTAANALCLGAMTPPWGNVYCHPSSHINNDE
CGAPEFYTNGAKLVAVDGPSAKIDVEKLRAATRVKVGDVHSTQPACVSLTQATEVGSL
YTLNEIEAIGQLCKDARIKLQMDGSRFANALVSLGCSPAAMTWKAGVDALSFGATKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVRLRLEQACSLLSSRSKAIAEVAQEVGFYDQSHFNRAFRQAFGVAPSHYQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EHTKGALSPAQWQRVRDYCFAHAGERITLDDLASLCALGRFQFLKQFKQTVGMTPHAW
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                                                                                                                                                                                                                                                             VVAAEATVLFDLSLAAEMGYRRKRAGHLFSKMRFLSAQTEAYLANDLWLRNARQANDM
ALRLARGLEGMHGASVLGATEANTVFCRLPSTLTENLLQAGFRFYHNRWEPNVVRFVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="RSp1116"
/EC_number="4.1.2.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="RSp1116"
/note="RS05504"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAD18266...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="PUTATIVE TRANSCRIPTION REGULATOR PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
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   complement(2462.
                                                                                                                                            predicted by FrameD*
                                                                                                                                                                                                                                     SFATTADDVDNLLRHMKAAAAGPSADTHATA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="RS05505"
35. .947
                                                                                                                                                                           /note="ACUR or RS05503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="Product confidence :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function="small molecule metabolism; degradation; amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function-"miscellaneous; not classified regulator"
                                                                                                                                                                                                                                                                                                                                                                                                             translation="MNRDPMPTTRTPALGFTSDNIEGASPEVLDAILAANAGQAAPYG"
                                                                                                                                                                                                                                                                                                                                                                                                                                           'db_xref="GI:17431590"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'protein_id="CAD18267.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product-"PUTATIVE LOW SPECIFICITY L-THREONINE ALDOLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 2259
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4228. .4725
/gene="RSp1120"
/note="RS05499"
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/gene="RSp1119"
/note="RS05500"
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/gene="RSp1118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3188. .3595)
/gene="RSp1118"
/note="RS05501"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mndaslhetiiscflehqrptvreiaerfnrdeaqvrqalral
adnhgvvlhphsdevwiahpfsaapttcvvksgnrkwwgncawcalglvhlaggsati
etrigaiddhviiriengrlldtdyvvhfpipmkhawdnviytcsvqllfrdeaqvde
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                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mgwsevgetvcpiartlavvgdrwtvlilrelflgvkrfeefqa
QTGMSSHLLSTRLKRLEADGIvvrhlySDRPPRHEYRLTSKGLDFYPLLLSLKSWGEK
WGGFKAKTAPALTITHRQCGHETGLKLVCPACDEPFGPKDATVTLGASFKAERQARRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene name confidence : hypothetical
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/gene="RSp1119"
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aadntyhslcvqpvivlsgdqetlkavhrralerkvphglyiedmfstghDaanravf
aehgpdsarvvgialreekkiydkitkgarmhp"
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/protein_id="CAD18268.1"
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Gene name confidence : hypot
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/function="miscellaneous; unknown"
                                                                                                                                                                               Gene name confidence : hypothetical
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/db_xref="GI:17431591"
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                                                                                                                                                      predicted
                                                                                                                                                                                                  /gene="RSp1120"
/function="miscellaneous; hypothetical/global homology"
/note="Product confidence : hypothetical
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/note="Product confidence : hypothetical
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note="Product confidence : hypothetical
/product="CONSERVED HYPOTHETICAL PROTEIN"
                                                                                             predicted by Codon_usage predicted by Homology predicted by FrameD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="CONSERVED HYPOTHETICAL PROTEIN"
/protein_id="CAD18270.1"
/db_xref="GI:17431593"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="CONSERVED HYPOTHETICAL PROTEIN"
'Protein_id="CAD18269.1"
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                           /transl_table=11
                                              /evidence=not_experimental
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by Codon_usage
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TTCGACCGCCGCCTCTACCCGCCCGCCGCCGCCACCGAAGAGATCATCGAGGT
                                                                                                                               CGGCCACACGGCGCTGCGCAACAACCACCTCGACCGGCTCGACCGCCCCGCCCACGGCGCC
                                                                                                                                                              GGGCCATTCAACGCTGCGCGCGCGCGTCATGCCGGACTTGCAGCGCGCCGCCGCCACCGACGA 533
                                                                                                                                                                                                                                                                               CAACCCGCCCGCCCCTGGACCTGCTGGACGAGGCGCTCTTACCGTTTCGAGCGCTT
                                                                                                                                                                                                                                                                                                                                                          CATCACCACCGTCATCGTCGGCAACTGCGGCATCAGCGCGTCGCCGGCCACGCTCCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCCACGACGACAACTACCTGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAGGG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTCGCCATCGCCGATGGCCGCATCGCCATCGCCACCTCCGACTCCACCGCCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCCGCAGGGTCCGCATCGTCGACGGCAGGCGGCCACGAGCCCGAGTCCACGCTGTTCGA 95946
                                                        CGAAGTCGAAGCCATGCGCGCGCAGCTGCGCGAGGCGCTCGACCACGGCGCGCTGGGCCT
                                                                                        GGAAATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCCATCGGCAT 593
                                                                                                                                                                                                                                            CGCCGACTACCTGGACGCGTTGCGGGCCACGCCGGCCGTCAACGCCGCCTGTATGGT
                                                                                                                                                                                                                                                                                                                                                                                           CGTCACCACGGTGGTCACGGGCAATTGCGGGCATCAGCCTGGCGCGCCGCTGGCGCAC---GC
                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCCACGACGACCAACGTGATCCGCACGCCGGACATGCTGCCGAAGGTGTCGCAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCGACCTGCTGCTGCGGGGGGCACCCTCATCGACGGCAGCAACACCCCGGGGGCGGCG 116
                                                                                                                                                                                                         al Similarity
876; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'translation='MAEKITTRKPRADAERNRQRLLDVAKTAFAEKGVSASLEDIARE
AGVGIGTLYRHFPTRDALIDEIYRDEGSFLAERARQLSEDQPPLEAVRQWILLFVGYL
ANKQIRADVLNCMTDCSERICTLSGEVLIETLAQLIERAKQSGAIGLAVEPLDILSAV
GOVASFGAELDWEAGARRLVEVMVAGLRVGAATGGKR*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Product confidence: putative Gene name confidence: hypothetical predicted by Codon_usage predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MPAITRHPRPGAPRYLEDFKVGDLTETSGFAVTRDMILSFAEQY
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PMRPGDVLRARAEVIAIRPSKSRPDRGFMDARVTTTNSEGVTLVTQRWSLVVPRRPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="PUTATIVE TRANSCRIPTION /protein_id="CAD18272.1" /db_xref="GI:17431595"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(5017. .5610)
/gene="RSp1121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKVAF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="RSp1122"
/note="RS05497"
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                                                                   GCCGATCTCGTGCTGTTCGACCCCGACACGGTGCGCGACCTCGCCACCTTCACCGACCC
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CGGTGCCGTGCAGCCGCGCGCGCGCGCGCGCCTTCCTGCGGCGCGGGCC
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REFERENCE AUTHORS KEYWORDS SOURCE ORGANISM ACCESSION VERSION RESULT AFAA6 DEFINITION rocus AFAA6 Alcaligenes xylosoxydans --'Ahhvdrolase, complete Alcaligenes xylosoxydans (strain A-6) DNA, Achromobacter xylosoxidans D50061.1 GI:769683 N-acyl-D-amino acids amidohydrolase amidohydrolase, D50061 Achromobacter Bacteria; Proteobacteria; (bases 1 to 1467 Cds beta subdivision; for N-acyl-D-amino DNA clone linear Alcaligenaceae; ar BCT PAGD 10-FEB-1999

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                                                                                                                                                            TGTACTTCGGCGCGCTGGAGGCGCAGCGGCCGATGATCAACGTGGCCGCCCTGGTGGGCC
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                                                                                                                                                                                                                                                            CGCCCGCCCCCTGGACCTGCTGGACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCGCCG 418
                                                                                                                                                                                                                                                                                                                           TCACCACGGTGGTCACGGGCAATTGCGGCATCAGCCTGGCGCGCTGGCGCACGCCAACC 358
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Submitted (06-MAR-1995) Mamoru Wakayama, Oita University, Chemistry; Dannoharu, Oita, Oita 870-11, Japan (Tel:0975-69-3311(ex.746), Fax:0975-69-7957)
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LDIYPYPGSSTILIPERADQIDDIRITWSTPHPECGGQSLAEIAARMGCDAVTAARRL
CPAGAIYFAMDENEVRRIFQHECCMVGSDGLPNDAHPHPRLMGSFTRVLGRYVREAEL
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EHVLVNGCAVFPQAPPSHRPGRILRRDASIAGAPEFSR"
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ADRRLDAGGRIVAPGEIDTHGHDLMFVEKPGLEWKTSQGITSVVVGNCGISGAPAPL
PGWTAAALALLGDSPLFADMANYEGALEAQREWINVAALVGHANLRLAAMRDPAAQPS
AKEQRAMERMLADALEAGAVGESTGLAYQPGGVAEQAELDGLARVAAARGALHTSHIR
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/product="N-acylop-amino acids amidohydrolase"
/protein_ide"BAA08778.1"
/db_xref="GI:1707291"
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Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Kroph et al., Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colney, No
On May 9,
Notes:
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Streptomyces coelicolor A3(2).

Streptomyces coelicolor A3(2).

Streptomyces coelicolor A3(2).
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2 (base
                                                                                                         jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web. (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor sequencing at The by the BBSRC and Beowulf Genomics Details of S. coelicolor sequencing at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission Submitted (31-MAY-2001) Streptomyces coelicolor sequencing
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for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SC2K36
Streptomyces coelicolor
AL591857 AL645882
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for
                                                                                                                                                                                                                      http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION:
                                                                                                                                                                                                                                                                               Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cerdeno, A.M., Parkhill, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished 3 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O'Neil,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL591857.2 GI:20520740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 22251)
Redenbach, M., Kieser, H.M.,
                                                                                     upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H. and Hopwood, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 to 22251)
and Harris,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
to
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r cosmid :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Denapaite,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2K36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eichner, A.,
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we arrange for
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                                                                                                            choose the most
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FEATURES
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overlaps cosmid SCK15 and cosmid SCK13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene-"25CK36.02"
/note-"25CK36.02, probable phosphoenolpyruvate
/note-"25CK36.02, probable phosphoenolpyruvate
carboxykinase, len: 609 aa; similar to SW:PPCK_CHLLI
(EMBL:556812) Chlorobium limicola phosphoenolpyruvate
carboxykinase [GTP] (EC 4.1.1.32) PckA, 646 aa; fasta
scores: opt: 2400 2-score: 2689.0 bits: 507.7 E():
3.6e-142; 58.361% identity in 598 aa overlap. Contains
Pfam match to entry PF00821 PEPCK, Phosphoenolpyruvate
carboxykinase and match to Prosite entry PS00505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein, len: 234 aa; similar to SW:YA85_MYCTU (EMBL:AL021897) Mycobacterium tuberculosis hypothetical 26.0 kDa protein Rv1085c or MTV017.38c, 242 aa; fasta scores: opt: 563 Z-score: 653.6 bits: 128.3 E(): 8.6e-29; 39.524% identity in 210 aa overlap. Contains possible
                                                                                                                                                                                                                                                           RTMTRMGQPVLDELGDEGFFVKAVHSVGAPLEPGQADVPWPCNSTKYISHFPEDREIW
SYGSGYGGNALLGKKCYALRIASVMARDEGWLAEHMLYLLKTEPFGAPKYVAAAFPSA
CGKTNLAMLEPTISGMTVETIGDDIAMMRFGEDGRLYAINPEAGFFGVAPGTGEHTNA
NAMKTLMGNSVETNVALTDDGDYWWEGMTEETPAHLTDWKGNDWTPESCTPAAHENAR
FTTPAAQCPIIAPEWEDPRGVPISAILFGGRRATAVPLVTESFDWNHGVFLGANVASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(160.
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                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MARDIAAPPYPTNHQELISWVNEIAELTQPDAVVWCDGSEAEYE
RLCGELVEKGTFRKLDPIKRPNSYYAASDPTDVARVEDRTFICSAKEEDAGPTNHWKD
PAEWRAIFTGDKGEGGLFRGSMRGRTMYVVPFCMGPLGSPLSALGVEITDSAYVAASM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLIIAGTYTPLTMLLLPGAKGEWLLWGIWAAAAAGIVFRVFWVGAPRWLYTPCYLAMG
WAAVFYLPEFMRAGGVAVLVLVIVGGLLYSAGGVIYGLKRPNPSPRWFGFHEVFHSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative integral membrane protein"
/protein_id="CAC40591.1"
/db_xref="GI.14285272"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphoenolpyruvate carboxykinase (GTP) signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hydrophobic membrane spanning regions"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="cosmid 2K36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:100226"
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                                                                                                                                                                                                       KTAAAEGKVGELRRDPFAMLPFCGYNMGDYMGHWVDVAKDKDQSKLPKIYYVNWFRKD
DAGRFVWPGFGENGRVLKWIVERLEGRADGVETPIGVLPTKESLDTDGLDLADADLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative phosphoenolpyruvate carboxykinase"
/protein_id="CAC40592.1"
/db_xref="GI:14285273"
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/translation="MTASVPDAPRDLPAGGRGPVTLSLPHPVKPKLRGWLHLGMPPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="2SCK36.01c, conserved hypothetical membrane
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                                                                                                                                                                           LLSYDKEVWREEAALVPEHLNTFGDHTPAELWDQYRALVRRLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="SPTREMBL:Q93JL5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                          /note="Pfam match to entry PF00821 PEPCK,
Phosphoenolpyruvate carboxykinase, score 1344.70, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                 'gene="2SCK36.02"
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Best Local
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10533 CCGGGACCCAGGAGGAGTCAGGCATGGAAGAGCTGGTCATCAGGGACGCCGACGTCGTGG 10474
                                                     CCATGTCCCAATCCGAGTCCCAGCCCTTCGACCTGCTGCTCGCGGGGGGGCACCCTCATCG 91
                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aa; N-terminal region presents low similarity to
N-terminal region of TR:O14362 (EMBL.721911)
Schizosaccharomyces pombe putative glucan synthase-1 (EC 2.4.1.34) SPBC30D10.17c, 504 aa; fasta scores: opt: 176 2.4.1.34) SPBC30D10.17c, 504 aa; fosta scores: opt: 176 2.5 core: 188.3 bits: 44.3 E(): 0.0071; 24.9318 identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="Sptrembl:Q93JL3"
/translation="MSSIHDEATWEPLLRURASHPERLAGPGGHVMGQIGLGGWSVPVrtanslation="MSSIHDEATWEPLLRURASHPERLAGPGGHVMGQIGLGGWSVPVRTHPHAPGGAASLYEMQDDEFTAVEAVQAALRAHGRQSVSFMVETRVDGRTALHVVDS
VRVEHHGLVSPEYGTLVLYEGAVPEPWRRLPEAVPGALPAPSADPALLERTLRERLPD
AVGATEAEIAEAQTRLGVTLPDELKALYRVVRARWQDWRGDYAAQERVVDAVGCELLP
LDQLYVADARSRPCLMQFAATDAAVTAPDAAVQGLYGSPGWIAFGDNGGGDRLALDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 aa overlap and C-terminal region to C-terminal region of TR:AAK22951 (EMBL:AE005774) Caulobacter crescentus oxidoreductase, GFO/IDH/MOCA family CC0967, 307 aa; fasta scores: opt: 146 Z-score: 160.2 bits: 38.4 E(): 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="2SCK36.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mSGDGLEGLLAAVHRLTAQRMGPPVCGTAGHGTGHVCLVPPAGA
GLPGIEEAIGSRFGEPLRLVTGTTTEAAGGSAGLPLRTPFGERIVEMRAWAYGDRWIG
CGTVRADDADGAVRPVVLVAERADPAAGASAPATWVDGIVAVTGWETARARAVDWPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (4210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGPGGHTGQVVMIGHEDSIGAGLLAESLTDMVVNGRAEMHPGRDWDRPPVVARLNVLG
DDVSAVARPELEVLVLGGREGEPRSLAPLAGLPRLRTLHACPGALADPLEIAGLTRLE
YLRLGPEEMRVLLDAGAVPRSLLAAHIEVRGEHHPPRIIALANELLSLMDRPLISRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRLWEPYPYYPAPGGLLQWASTEQADGFYWLTGDPDPDRWPYLAKEDYPDSWERFDGP
                                                                                                                                                                                                            /product="putative membrane protein"
/protein_id="CAC40595.1"
                                                                                                                                                                                                                                                                                             Contains possible /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (5618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative bif
/protein_id="CAC40594
/db_xref="GI:14285275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scores: opt: 146 Z-score: 160.2 bit
26.590% identity in 173 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="2SCK36.04c"
/note="2SCK36.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="SC04981"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMBL:Q93JL4"
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/protein_id="CAC40593.]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="SC04980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="PS00505 Phosphoenolpyruvate carboxykinase (GTP)
                                                                                                                                                                                                                                                                                                                                                                                                     /note="SCO4982"
801. | see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db_xref="GI:14285274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transl_table=11
                                                                                                                                                                                                                                                                                                                                                                            5801. .5983
/gene="2SCK36.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JEGDLDTDRTAQGGAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="2SCK36.04c, possible bifunctional protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="2SCK36.03c,
                                                                                                                                                                                                                                                                    transl_table=11
                                                                                                                                                                                                                                                                                                                                                  note="2SCK36.05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=
                                                                                                                              9.8%;
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Pred. No. 1.5e-1
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5610)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4213)
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                                                                                                                                                                                                                                                                                                                         putative membrane protein,
hydrophobic membrane spann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bifunctional protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein 2SCK36.03c"
                                                                                                                                                          DB 1;
                                                                                                          647;
                                                                                                                                                            .Length
                                                                                                          Indels 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aa 
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                                                                                                       Gaps
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	1034TGGTGCCCGAGCTGCAGC 1051	ΥO
misc_feature	9456 CCGGCACGGCGACCCCGGCGCTCGCCGAGTACGTCGGCCGCACGGTGCTGGAGTCGGCGC 9397	문
	1004 CGGCCGAGCGCGGCAAATCCAAGTACGACG 1033	Qy
. outce		
		Q
TITLE Direct JOURNAL Submit	914 AGCAGGACCGCTGCTGCCGGGCGGACGCATCATCACCTGGTGCAAGCCCTTCCCCC 973	Db Qy
PUBMED 120607 REFERENCE 2 (ba AUTHORS YU, T	9636 CCCCCGGCTGCACCCTCGTGGCACTGCTGCCGAGCTGGGCGAGCGA	рь <i>4</i>
JOURNAL Proc. MEDLINE 220560		
TITLE The bi	836 CGCTGATCGAGGCCGCCATGGCGCGCCAGGACGTCTCGCTGGACGCGTATCCCTACG 892	Qy
REFERENCE 1 (ba	776 TGATCTCGCACCACAAGGTCATGGGCCAGCCCAATTTCGGCCGCTGGCGGGAAGACGCTGC 835	D Qy
ORGANISM Actino	GGCCCTGAAGGCGTACGAGGACATGGTGGAGCTGACCCGGGAGGCGGCTGCCCCCTGC	
DS N	716 ACATCGTGGCCGCGCTGGAGGAAACCTTCCGGCATCGCCGCGAGCTGGACGTGCGTG	
ON CN	656 GCCGGCCGTGAGCGCGATGGCGGCATCTACGCCACCACATGCGCGACGAAGGCGAGC 715	P &
	GTCGGGGCTGACCTACACGCCGGGATGTACGCCAAGGACGCCGAGCTGACCGACC	
DECITE 12		Q,
Qy 1472 CACGCACG Db 8916 GCCGGGTT	536 AAATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCGGCATTT 595	Db .
8976	476 GCCATTCAACGCTGCGCCCCCGCGTCATGCCGGACTTGCAGCGCCGCCACCGACGAGG 535	ду рь 1
Db 9036 CGGGCAGC		
QY 1352 ATACCGCC		Qy
Db 9096 GTCTGGTC	359CGCCCGCCCCCTGGACCTGCACGACGACGGCTCTTACCGTTTCGACCGCTTCG 415	Оу рь 1
9156	314 CGGGCAATTGCGGCATCAGCCTGGCGCCGCTGGCGCACGCCAACC 358	Qy Db 1
9216	254 ACCTGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAGGGGGTCACCACGGTGGTCA 313	Qy Db 1
9276	194 ACGTGTCGGGCCTGGTGGTCGCCCCGGCTTCATCGACTCGCACACCCACGACGACAACT 253	Оу рь 1
9336	152 CLANGGGGATGTGTCGGACGCCGCGCGCACACCCG	р (Ş
Db 9396 GGCTGCGC		-
-	92 ACGGCAGCAACACCCCGGGGGGGGGGGGGGGGGGGACCTTGGGGCGTGACCGGGGACCGATCGCGATCGACCGATGATCGCGG	QV

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TTCCGCGCTGAGCCCGG 8894
                                                                                                                                                   CCACCTTCGAACACCCTACCGAGCGCGCGCGCGGCATCCATTCCGTGTACGTCA 1411
                                                                                                                                                                                                                                                           GETGGCCCACCTCACCTCACGCCGCCGCCGCCGCTGCGGCTGCCGACCGGG
                                                                                                                                                                                                                                                                                                                          SECCECCTEACCCCE 1494
                                                                  CTCGTTCGACGAGCCGCGGGTGCTGCCTACGGGCATCCCGTACGTGCTGGTCG
                                                                                                                                                                                                                                                                                         GGTATGGAAGATGACCGGCCTGACCGCCGCGCGCTTCGGCCTGGCCGGGCGCG 1291
                                                                                                                                                                                                                                                                                                                                                                                          CATGATCGGCTCCGACGGCCTGCCGCACGACGAGCGCCCGCATCCGCGCCTGT 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATCCTCCAGCACGTCGGCCACGAGGAGAACGTGCGCGCGATCATGCGGCACC 9277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCCATCTACTTCATGATGGACGAACCCGACGTGCAGCGCATCCTGGCGTTCG 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCGAGAGCCCGTGGACGGTCGCCCGGCACCTGCTGCTCGCCGACCGGCTGG
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DEFINITION

Actinosynnema pretiosum subsp: auranticum maytansinoid antitumor agent ansamitocin biosynthetic gene cluster I, partial sequence.

VERSION

AF455501

KEYWORDS

SOURCE

ORGANISM

Actinosynnema pretiosum subsp. auranticum.

ORGANISM

Actinosynnema pretiosum subsp. auranticum.

Actinosynnema pretiosum.

Actinosynnema pretiosu

/note="cluster I of the maytansinoid antitumor agent ansamitocin biosynthetic gene cluster" $\,$

/db_xref="taxon:42198"

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CDS
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AELSREHWTYLNTDYQQDVLRAWSAQGCLAEVTAKLGYRFTLRDSVFPTTTTRGAALP
VRVNLTNDGYAAAVNQRTVNLVLRNTTTGALTRLPLTADPRTWLPGARAIAQDAQIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEDAARVAGVKLVLRFAYTASESGEDAPKERVLAHIDQLAPLLRANADVTAVVQAGFV
GAWGEWYYTKNEGNAGVVSATDQANRKAVVDKLLTALPADRAVQLRTPKFKRALYGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLATGQYALLLELADPALPGRPEYSIQTANTGLWDARTGLNDLKQTITVS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARWTVERADLGEQASPNDVDVVFQVEAPVETSAKVTHTYTAGAGGSVAYQPSSANVPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAFSRVYVDTDRSAATGYAQGGIGADHLLENGSLYRHSGGGWAWTQVRTVPFTSASGV
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/db_xref="GI:21449383"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3450.
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                                                                                                                                                                                                                                                                                                                             /translation="marrnperraalldaavevlagegarglifravdoragvpagta
SNYFAGABEILTGAGERVYORLDOAFLGETPDGFRORSRVTEMMALVDRVSAFPTG
FLALLELRLEAARNPELFETLTARVRADLERVBAHBASGLFODGTTVALLWLALNWL
ILERLTLPDLLTDHORRDLVTALVDRLLAGOPEEAGSPFDESGK"
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LLLTARFVQGIGASAAAVLVFVIIGDRYRGPAALRMYGLVNAAMSALMTCAPLLGGAI
NRVAGWRGNYLAVCATTALSLLLVFLFLPETRTRARTAITARSVLADYRRLLGSRAYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MYTASAVLCARAGCGAPRPAGATARWRFCSTACKQAAYRLRRKA
GSASHEHEDEQLREALLALVARARTLTEATPPWSAQATALVGLARRVVELAAARDAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="asm37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="asm35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11
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PTHVRPLVGMPLDTPNRRYDTVLMGRGSYQPALDAGVGSPYAHLRQYVVSRSLPDADP
AVALVRADPVGLVRELKREDGLDVWLCGGADLAGQLLPEIDELVVKTYPVVAGGGTPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FPELAGAASSATMGLRALLVTLLTALAGALSTGGPFAPAAVMAGAVAAVVLLSALSPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JLGGPAGAVRWGLGAVVVGVLGFLLLGDGPVAVTGSVALFCVGFAVCYPVVFDRSMSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NASLTPSLLFAAYLVFIAASPFLYTAAFGLGVTGFALHLLVVVASFAVPSAFATGIIP
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                                                                                                                                                                                                                                                  /gene="asm33"
1151. .4723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transl_table=11/
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                                                                                                                                                                   transl_table=11
                                                                                                                                                                                          codon_start-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSLYVRARPRADRYGATATVETVVPHQVPATHRHGTPLHVFYGSNGGSGEGLARTIAG
DGAARGWATSVAPLDDAVRALPASGPVVIVSSSYNGAPPDNAAHFVRWLTQDGPDLSG
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PPESFRPPADNTVPVVLIAAGTGIAPFRGFLRARAALGGEPGPALLLFPGCRGPELDDL
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SANADSRARSRGRDPRTSLNRSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGFAPRAFRPVDVRAFDHGGVVTTYRPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QHPARSRGLEGYLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FKFSTYATWWIRQAITRALADQSRTIRLPVHMVEVVTKLARIERDLLHRNGREATAEE
VAVELDVTPEKVVELRQHARTPVSLDQTIGAEADTSIGDLIADENAVAPLEAVSSALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVVRDGQRAKDHLLEANLRLVVS.TAKRYTGKGMALLDVIQEGNLGLVRAVEKFDYAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MWIGYSADGRRRRPVRWWGVTEAFTWETDEDIKLAATLRRDAEA
ANAADSTRAYLKAIGRVRLLTADQEVELARRVEAGLYAEHLLDLPPAARGSRRPVELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="RNA polymerase sigma factor"
/protein_id="AAM54109.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5415 .6461
/gene="asm31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAM54110.1"
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Cfrskqelytallytglntsldaampaispdlpavdnvrtmlaafmtafqadpeaelv
Lgelytlagepeleelpamphreyvakavahldrlaeeagfdysvdrallaelvvsv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKAHRLLMPAFGPTAMRDHFPAMLDIAEQMLVRWRRFGPDHRIDVADDMTRLTLDTIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAEEFAALGDWLEVDRAYSRHPDGEVRHVQHRLWQRRDRVRELVDAGARVYLCGDATR
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IPACAWMPFGHGARACIGRPFALQEATLVLALVLQRFDLALADPDHRLTIKQTLTLKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="cytochrome F
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     /gene="asm28"
/codon_start=1
                                                                                                                                                                                                                                                     /protein_id="AAM54107.
/db_xref="GI:21449375"
                                                                                                                                                                                                                                                                                                         /transl_table=11
/product="transcriptional regulator"
                                                                                                                                                                                                                                                                                                                                                                                           /gene="asm29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGPAVEEVLGRIGPGAGWLDALRAGGRYATDVF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _CAFGARFNŚFYRDRAHPFVDAMVRSLVEAGERAERLPGVQPFLVGRNQRYRDDIATM
VRIADGIVAARAALPAGERPDDLLERMLTCADPVTGERLSARNVRYQLATFLIAGHET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [VALTFAGQRQVFASSHELVARMCSDPSWGKAVHPALEQVRDFAGDGLFTARGDEPNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MVATGTRIPGPKPLPLVGNLLDVLTSDLDTDVDFLDRCHREHGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="GI:21449376"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="asm30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="asm30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein_id="AAM54109."
db_xref="GI:21449377"
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                                                          /gene="asm28"
10393. .10857
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                                                                                                                    .0393
                                                                                                                                         DGVASSWFSHRDGELAKASLDQFAVMFAALTR
                                                                                                                                                                                                                                                                                                                                                                codon_start=1
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TGGTGATCTCGCACCACAAGGTCATGGGCCAGCCCAATTTCGGCCGCCTCGCGCGAGACGC
                                                                                                                       ACATCGTGGCCGC---GCTGGAGGAAACCTTCCGCATCGGCCGGGAGCTGGACGTGCCGG
                                                                                                                                                                                                                       CGCGCACCTCGGCCCACCCCCCCCCCCCCCCGAGCCGCGTCGACCCGTGGT
                                                                                                                                                                                                                                                                                                 CGCTCACCGCCTCCCGCCGCCCACAACCCTCCACGCCTCCGCCCCCGCACACCTCCGCCC
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complement(10912...11937)
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/protein_id-"AAM54105.1"
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/product="unknown"
/protein_id="AAM54106.1"
/db_xref="GI:21449374"
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DEFINITION ACCESSION

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                                                                         AGCTGGGCCAGATCGCCCTGAGCTACGAGAAGCT 1757
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alpha-amylase; glgBI, 1,4-alpha-glucan branching enzyme; glgP, glycogen phosphorylase; integral membrane transport protein; pfk2, 6-phosphofructokinase; pta, phosphate acetyltransferase; secreted nucleosidase; sodium:dicarboxylate symporter; transcriptional regulator; trxA2, thioredoxin; two-component sensor kinase/sensor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor sequencing at The Sanger Centre is funded
by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colney, Norwich, Norfolk NR4 7UH, UK
On May 9, 2002 this sequence version replaced gi:6941966
Notes:
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Submitted (03-FEB-2000) Streptomyces coelicolor sequencing project, Sanger Cetre. Hinxton, Cambridge Sanger Cetre. Cetre. Sanger Captolor Sequencing project, CB10 1SA E-mail: barrellesanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              numbered using the following system coelicolor), 7B7 (cosmid name), .01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. 1 (bases 1 to 28751)
                                                                                                                                                                                                                                                                                                           sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 6All Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prediction is based on positional base preference in codons using specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinashi,H. and Hopwood,D.A.
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                                                                                                                                                                                                                                                  genomic
                                                                                                                                                                                                                                                                                                                                                                                                 upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 28751)
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                                                                                                                                                                                                              and overlaps with cosmids 8F4 and 3D11 on the AseI-B restriction fragment.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Harris, D.
                                                                                             /strain="A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                     /organism="Streptomyces
/note="Nominal overlap with Streptomyces coelicolor cosmid
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                                                                                                                                                        coelicolor A3(2)"
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(first CDS), c
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TRNEW:CAB51967 (EMBL:AL109661) Pfk, 6-phosphofructokinase from Streptomyces coelicolor (342 aa) fasta scores; opt: 1251, z-score: 1437.4, E(): 0, 56.7% identity in 342 aa overlap. Contains two Pfam matches to entry PF00365 PFK, Phosphofructokinase and Prosite match to PS00433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="arigulfaggdopglaayirsvyhravdayagdevigfeedotagl
ldgryraldlaavsg larggtilgssrlerdrilreachagdmigafgidalipigg
egtltaarmledaglevvgvpktidhdisstdrtegpdtavgvateamdrlkttaesh
grvmvvevmgrhagmialesgmaagahgiclperpfdpadlvkmveerpsrgkkfavv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aa) fasta scores; opt: 1274, z-score: 1463.6, E(): 59.1% identity in 342 aa overlap. Also similar to TRNEW:CAB51967 (EMBL:AL109661) Pfk, 6-phosphofructus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="SC6A11.02, pfkA2, 6-phosphofructokinase, len: 341
aa; similar to many e.g. SW:Q59126 (PFP_AMYME)
6-phosphofructokinase from Amycolatopsis methanolica (352
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acetyl/butaryl transferase, score 460.50, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Pfam match to entry PF00365 PFK,
Phosphofructokinase, score 278.20, E-value 1.6e-101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEAESVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CVAEGAHPAEGSMDYGKGAIDKFGHERFQGIGTALAFELERRLGKEAKPVILGHVQRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphofructokinase signature*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="6-phosphofructokinase"
/protein_id="CAB72402.1"
/db_xref="GI:6941968"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          database similarities"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphofructokinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2121. .2804
/gene="SC6A11.02"
/note="SC6A11.04c, possible integral membrane transport
protein, len: 296aa; similar to many proposed transport
proteins e.g. TR:Q9X9Y6(EMBL:AL096743) putative integra
                                                                   /gene="SC6All.04c"
/note="creation"
                                                                                                                                                  /gene="SC6All.04c"
/note="scosico"
                                                                                                                                                                                                                                        RDFLDRIVDHFWTAVERHP"
                                                                                                                                                                                                                                                                                            EDVARAVGLGLPAYLRMEESDDWRGTDRQSAQLADVLGLTLPDFVTVTGREEKLADLL
                                                                                                                                                                                                                                                                                                                       /translation="mwrvrrpspgps0SGpppsnalaarrlraalnmgpehvahgirvs
YGLPYVSPDLVIAWERGTALPEGPELTALAGVLWCSPGELIGRPQSLREHRVAHGIRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical
/protein_id="CAB72403...
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/note="crf":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /qene="SC6A11.
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                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GI:6941969"
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                                                                                                                                                                                                                                                             SAVTTRWQGCVRPIAKLAPLDRRVLENVLQVLHQDYQGRMAATLSWGGGAPDSSAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="SC6All.03c, unknown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /butaryl transferase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .03c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry PF00365 PFK, score 52.20, E-val
                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        len:
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                                                                                                                                                                                                                                      CCGGGTCGACGTGTCGGGCCTGGTGGTCGCCCCGGCTTCATCGACTCGCACAC---CCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACGGTGGTCACGGGCAATTGCGGCATCAGCCTGGCGCCGCTGGCGCACGCCAACCCGCC
                                                          CACCCCGATGGGGCTGCGCCGCCGGCACATCACCAGCGAGGGCCGCACGGTCACCGC
                                                                                                                 CGACGACAACTACCTGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCAC
                                                                                                                                                                              CCCCGTCCTCATCGACTGGCGGGCCGGTGTCGCCCGCCCCTTCTACCTGGCCACCGGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane transport protein from Streptomyces coelicolor (298 aa) fasta scores: opt: 515, z-score: 609.9, E(): 1.5e-26, 33.9% identity in 295 aa overlap. Contains Pfam match to entry pr00528 BpD_transp, Binding-protein-dependent transport systems inner membrane component, Prosite matches to ps00402 Binding-protein-dependent transport systems inner membrane binding-protein-dependent transport systems inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Binding-protein-dependent component, score 53.20, E-complement(4248. .4334)
/gene="SC6A11.04c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Binding-protein-dependent transport systems inner membrane
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/gene="SC6A11.05c"
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complement(4870..5811)
/gene="SC6A11.05c"
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/gene="SC6A11.04c"
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VLPLAWVVLSALDPHASLRVKVPDGVTLDNFDAILTPEITFTPLLNSLILCGGATLLT
VVCAVLAAYPLSRFRSRLNRPFLLTILFATSLPITAIMVPVYALFVRVNMIDTMQGTI
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/protein_id="CAB72404.1"
/db_xref="GI:6941970"
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/protein_id="CAB72405.1"
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/note="piam match to entry pF00528 BPD_transp,
Binding-protein-dependent transport systems ir
component, score 53.20, E-value 5.7e-12*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 107.4; DB Pred. No. 0.0014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATCGTGGCCGCGCTGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGTGCCGGTGGT 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGAGCGCGCATGGCGGCATCTACGCCACCCACA-----TGCGCGACGAAGGCCGAGCA 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTCCTCATCGTCGGCCCCAACCCGGCCTTCCTCGGCTACATCGGCGAGGTGCTGCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGGACGCGTTGCGGGCCACGCCGGCGGCGGCCTCAACGCCGCCTGTATGGTGGGCCCATTC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGCGACGCCGTGCTCGCCGCGCGCTGAACTCCGCGCGCCACCGGCCGCATGGGCGACAT 17006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGCACGACGAGATCCTCGACCTCGGCGACGAGGAGGCGCACCGGCCACGAGGACCCCTC 16946
CTACCGAGCGCCGCCGCCATTCCGTGTACGTCAACGGCGCCGCCCGGTCTGGCAAG
                                                                                                                                                                                  CCGGCCTGACCGCGCGCGCTTCGGCCTGGCCGGGCGGCAGCTGCAGGCCGGGTACT 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGACCCCAGCGACATCACCCAGATCCGCGACGAACTCGCCGAGAACCCCCGAGGTCTGGTC 17645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCCTTCTACCCGCCGCCGCCGCCGCCACCACCGAAGAGATCATCGAGGTGTGCCGGCC
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                                                       CCTACGCGCAGGGCGTCCTCGACGTGTCGTACGCGTCCCGGCACCTACGAGTTCGAGGACA 17935
                                                                                              TCGCCGACCTGGTGGTGTTCGACCCGGCCACGGTGGCCGATACCGCCACCTTCGAACACC 1372
                                                                                                                                          CGGTCACCCGGCGCTGGACCGTCGCCGACGTGCCCCTGCTGGACGACGCCGCCGAACTGC 17815
                                                                                                                                                                                                                                                                                                                  CGCCC-----
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                       CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCAGACCGCGGAGGCGGCCGGTGTCGGCTCCTGGTCGAAGATCCTCGCCCCCTACGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAAGGAAGTGATGGGCGCGCGCCTGCGCGCCGAGCGCAAGGCCCCGGAAAATGACCCTGC 1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGCAAACCGCTACATGGCCCCTCCCTCCGCTCGCAATACGGCCCCACCCGATATCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nierman, W.C., Feldblyum, T.V., Laub, M.T., Paulsen, I.T., Nelson Eisen, J., Heidelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R. Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caulobacter crescentus CB15.
Caulobacter crescentus CB15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caulobacter crescentus CB15 section
                                                                                                                                                                                                                                                         Heidelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., Laub, M.T., Deboy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and
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                                                                                                                                                                                  Submitted (31-JAN-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete genome sequence of Caulobacter crescentus Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haft,D.H., Kolonay,J.F.,
Berry,K., Utterback,T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ermolaeva, M., White, O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases
                                                                                                                                                                                                                          Submission
complement(86. .892)
/gene="CC3444"
                                                                 complement(86.
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                                                                                                                                                                                                                                                                                                                                                                                                      1 to 14710)
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                                     /gene="CC3444"
                                                                                 /db_xref="taxon:190650"
                                                                                                    /strain="CB15"
                                                                                                                         organism="Caulobacter crescentus CB15"
                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., M., White, O., Salzberg, S.L., Venter, J.C., Shar
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ley,M.R.K., Ohta,N., Maddock,J.R.,
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359 of
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                                                                                                                                                                                                                                                                                                                                                                                 Eisen, J.,
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/product="hypothetical
/protein_id="AAK25406...
/db_xref="GI:13425162"
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PENVTLDNPGSNKNVCTVTIDYSQAPEQAQELANGLHDWATWENSPQLRLIRNDQTVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MTEDADLANFCCDELAEAVSPDANAGLIEHDSGLILLNLGEREE
EGETGVVLATIRFCPFCGTEIQTDEDIEAALGGVEETFN"
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                                                                                                                                                                                                                                                                                                                                             AILGMDELSEEDKLYVARARKIQRFLSQPFHVAEQFTNTPGAFVQLKDTIRSFKGIVD
GEYDHLPEGAFYMVGPIEEAVAKAEKMAAEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                        CALVYGQMNEPPGARARVALTGLSIAEYFRDEEGKDVLLFVDNIFRFTQAGAEVSALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="CC3446"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LREGKVTVKDGATTKVFDIQGGFADVGPEGLTILAEHAVEAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAK25407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="ATP synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MVLISAHKGCEGPSVGFNAVLSSCWGYLAYAPCARQPDRTRPRD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="identified by Glimmer2; putative"
                     YARRLASVIANLAAGVSGDGAPKLLAGTGRDDRHLVVVAAADRGLAGGFTSSIVRAAR
AHIDGLIAQGKDVRVVCVGKKVTAQLAKPYAGRIVETFDLSSYRQLTLSVAQPIADVI
TREYEAGETDVVTLFYSRFKSVVQQIPTGLQLIPAVVETGEAASGPTAVYEYEPSEEA
                                                                                                                                                                                                                                                                          complement(3196. .4071).
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/protein_id="AAK25408.]
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ILETLLPRNLTVQILSALLDNMAGFYASQMTAMDNATRNAGDMIKRYTLEYNRSRQAQ
                                                                                                                                        /product="ATP synthase F1,
/protein_id="AAK25410.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein_id="AAK25409"
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/db_xref="GI:13425166"
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                                                                                           translation="MASLKEMRNRISSVKATQKITKAMQMVAAAKLRRSQDAAESARP
                                                                                                                                                                                                                                                                                                                     lement(3196. .4071)
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Sequence 24, Appl	Sequence 4000, Ap	7.	Sequence 1, Appli			1,	, P	25,	1,	12, A				4006		4009	34	×		-	Sequence 784, App	Appl		Ξ.	Sequence 7984, Ap	

ALIGNMENTS

RESULT 1 US-09-976-059-1

Sequence 1, Application US/09976059 Patent No. US20020164747A1

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GENERAL INFORMATION:
APPLICANT: Farnet, Chris
APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2001-10-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (3118). (4032)
OTHER INFORMATION: ORF 2; positive strandedness
NAME/KEY: misc_feature
LOCATION: (4038)..(5048)
OTHER INFORMATION: ORF 3; positive strandedness
                                                               NAME/KEY: misc_feature
LOCATION: (7703)..(6693)
OTHER INFORMATION: ORF 5;
                                                                                                                               NAME/KEY: misc_feature
LOCATION: (6665)..(5814)
OTHER INFORMATION: ORF 4; negative strandedness
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OTHER INFORMATION: ORF 3;
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LOCATION: (2077)...(3078)
OTHER INFORMATION: ORF 1; positive strandedness
                       NAME/KEY: misc_feature
LOCATION: (9464)..(8130)
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OTHER INFORMATION: ORF 6;
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  negative strandedness
                                                                                                                                                                                                        strandedness
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NAME/KEY: misc_feature
LOCATION: (81909)..(81682)
OTHER INFORMATION: ORF 27; negative strandedness
NAME/KEY: misc_feature
LOCATION: (82346)..(82062)
OTHER INFORMATION: ORF 28; negative strandedness
NAME/KEY: misc_feature
LOCATION: (82587)..(84446)
OTHER INFORMATION: ORF 29; positive strandedness
LOCATION: (82587)..(84446)
OTHER INFORMATION: ORF 30; positive strandedness
LOCATION: (84481)..(85548)
OTHER INFORMATION: ORF 30; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (79864)..(78107)
OTHER INFORMATION: ORF 25; INAME/KEY: misc_feature
LOCATION: (81624)..(79861)
OTHER INFORMATION: ORF 26; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (70659)..(71906)
OTHER INFORMATION: ORF 19; P
NAME/KEY: misc_feature
LOCATION: (73439)..(71964)
OTHER INFORMATION: ORF 20; n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (65826)..(6530)
OTHER INFORMATION: OFF 15; F
NAME/KEY: misc_feature
LOCATION: (6546).:(67370)
OTHER INFORMATION: ORF 16; F
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LOCAFION: (15880)..(19035)
OTHER INFORMATION: ORE 12; p
NAME/KEY: misc_feature
LOCATION: (19032)..(39713)
OTHER INFORMATION: ORE 13; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (78110)..(76449)
COTHER INFORMATION: ORF 24;
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LOCATION: (75424)..(74213)
OTHER INFORMATION: ORF 22;
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LOCATION: (67384)..(70059)
OTHER INFORMATION: ORF 17;
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LOCATION: (15591)..(15863)
OTHER INFORMATION: ORF 11;
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LOCATION: (15203)..(13614)
OTHER INFORMATION: ORF 10;
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LOCATION: (11617)..(12802)
OTHER INFORMATION: ORF 9; negative strandedness
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LOCATION: (12751)..(10829)
OTHER INFORMATION: ORF 8; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (75535)..(76464)
OTHER INFORMATION: ORF 23;
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LOCATION: (74216)..(73563)
OTHER_INFORMATION: ORF 21;
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LOCATION: (70099)..(70662)
OTHER INFORMATION: ORF 18;
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LOCATION: (39713)..(65800)
OTHER INFORMATION: ORF 14;
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N: ORF 31; positive strandedness
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pil
FILE REFERENCE: 600, 438US1
CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR TILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                                                                         : SEQ ID NO 7
LENGTH: 1248
: TYPE: DNA
: ORGANISM: Streptomyces venezuelae
US-09-860-846-7
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                                                                                                                                                                Query Match 4.7%;
Best Local Similarity 44.2%;
Matches 439; Conservative
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                                                                      GCGTGCTCGCGGCCGATCCGCGGCGGCCGCCTGGCCGAGGTCGA-------CCCGC
                                          TCGCCCGCTGCCTGCCCCCCACG 47615
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                                                                                                                                                           Score 81.8; DB 9; Length 12
Pred. No. 4e-07;
0; Mismatches 542; Indels
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                   983 GGCGCGACCTGGATGAAGTCGCGGCCGAGCGCG 1015
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APPLICANT: Sherman, D.H.

APPLICANT: Liu, H.

APPLICANT: Liu, H.

APPLICANT: Zhao, L.

APPLICANT: Zhao, L.

TITLE OF INVENTION: DNA encoding methymycin an FILE REFERENCE: 600.438US1

CURRENT APPLICATION NUMBER: US/09/861,289

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: 09/105,537

and

pikromycin

RESULT 3 US-09-861-289-7

Sequence 7, Application US/09861289 Patent No. US20020110897A1

GENERAL INFORMATION:

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LENGTH: 1248
TYPE: DNA
ORGANISM: Streptomyces
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Best Local
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Local Similarity 44.2%;
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AGGACGTCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACC 922
                                                          TCGGCCGCTCGCGCGAGACGCTGCCGCTGATCGAG-----GCCGCCATGGCGCGCC
                                                                                         ACCGCGACCTCGTCATGGAGGTCCTGAAGGCCGAAGGCGTGCACACCCGCGCCTACTTCT
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                             CGCCGGGCTGCCACGAGCTGGAGCCGTACCGCGGGCAGCCGCACGCCCCGCTGCCGCACA
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Pred. No: 4e-07;
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Matches 439; Conserv
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Best Local
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CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT:
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TYPE: DNA
ORGANISM: Streptomyces venezuelae
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TGGCCAGCGGCGCATCGGCATTTCGACCGGCGCCTTCTACCCGCCGCCGCCGCCGCCGCA 631
                                                                                                      TCACCGACGACGCCGACCTCGCCGCCCCGGATCCGCGCCCTCCACAACTTCGGCTTCGACC
                                                                                                                                          CCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCGCCGCGGTCATGCCGGACT 511
                                                                                                                                                                                                                                                  ACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATTGCGGCATCA
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                                                                     TGCAGCGCCGCCACCGACGAGGAAATCGCCGGCCATGCGGGACCTGGCCGAGGAAGCCA 571
                                                                                                                                                                             AGGTCTTCAGCTTCCA----CGCCACCAAGGCCGTCAACGCCTTCGAGGGCGGCGCCGTCG
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Xue, Y.
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Pred. No. 4.3e-07;
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Best Local Similarity
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Patent No. US20020110897A1
                                                                                                                                                                                                                                                                                                        LENGTH: 13613
TYPE: DNA
ORGANISM: Streptomyces
-09-861-289-3
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                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
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CURRENT FILING DATE: 2001-05-18
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TCGCGCCCGGCTTCATCGACCACCCACCACCACGACAACTACCTGCTCAGGCGTCGCG
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Pred. No. 4
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US-09-860-846-1
Sequence 1, Application US/09860846
Patent NO. US20020164742A1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SEQTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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pikromycin

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                                GACGTCACGGTCCTCCCGCTGCGCGCGCGCGCGCCCCGAGCCCCGAGACCCTCGCCGCC
                                                              TGGTGCAAGCCCTTCCCCGAACTGAGCGGGCGCGACCTGGATGAAGTCGCGGCCGAGCGC 1014
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Pred. No. 1.3e-05;
0; Mismatches 747;
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1 \,
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APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.4380S1
CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
CURRENT FILING DATE: 2001-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
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                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                  4979 CTCGAACACCACGGCCTCGTCCCCGACCTGCTCACCGGCCACTCCGTCGGCGAGATCGCC
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 GCCGACTACCTGGACGCGTTGCGGGGCCACGCCGGCGGCGGCCGTCAACGCCGCCTGTATGGTG
                                                                                                                                       GGCGTCACCACGGTGGTCACGGGCAATTGCCGGCATCAGCCTGGCGCGCCGCGCGCACGCC 354
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                                                                   AACCCGCCCCCCCCCGGACCTGCTGGACGAAGGCGGCTCTTACCGTTTCGAGCGCTTC
                                                                                                      GACCTCACCGCGTACACCCAGCCCGCCCTCTTCGCCTTCGAGGTGGCGCTGTTCCGCCTC
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Pred. No. 1.3e-05;
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       GCCGCCTGAGCCCGGCGCGAGCCCTTACAATCCGGCG
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                                                                                                    TTCCTGGAGCTCGCCCTCGCGGCGGGCGACCACGTCGGGGCGGTCCGGGTGGAGGAACTC
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TIFILE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS
FILE REFERENCE: ARCD:317USCI
CURRENT APPLICATION NUMBER: US/09/825,288A
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/259,821
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 08/690,473
PRIOR APPLICATION NUMBER: 08/690,473
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
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US-09-825-288A-1
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Best Local
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TYPE: DNA
ORGANISM: HERPES VIRUS,
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Local Similarity 42.68;
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                             GCACCAAGGTCATGGGCCAGCCCAATTTCGGCCGCTCGCGGGAGACGCTGCCGCTGAT
                                                                                                                                                                             GCTGAGCGCGCATGGGGGATCTACGCCACCCACATGGGGGAACGGAAGGCGAGCACATCGT
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                                                                          GCGCGCCGCGGTCATGCCGGACTTGCAGCGCGCCGCCGACGACGAGGAAATCGCGGCCAT
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Pred. No. 1.5e-05;
0; Mismatches 766;
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US-09-815-242-4056
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FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                      APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                 APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
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Trawick, John D.
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Zyskind, Judith W.
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR ELLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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LENGTH: 3189
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
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Pred. No. 2.2e-05;
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1033 CACACCCTGTTCGAAGCCCTGGTGCTGGTGGTGGTGGTGATCCTGTTCCTGCAGACC

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FITLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.438US1
CURRENT APPLICATION UNMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
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TYPE: DMA
ORGANISM: Streptomyces venezuelae
-09-860-846-30
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APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
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                                               GACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCCGACCGGCGCCCTTCTAC
                                                                                   AGCATCATCGGGGCGAGCAAGTTCGGCGGCCTCTCCCCCGACGGCCGCGCCTACACCTTC
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GCGCGCCA 863
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Pred. No. 2.5e-05;
0; Mismatches 493
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 30
LENGTH: 13842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30, Application US/09861289 Patent No. US20020110897A1
                                                                                                                                                                                                                                                                                                                                     Matches 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
APPLICANT: Dao, L.
TITLE OF INVENTION: DNA encoding methymycin
FILE REFERENCE: 600.438US1
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                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Streptomyces venezuelae
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Pred. No. 2.5e-05;
0; Mismatches 493;
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Patent No. US2002016474ZA1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
                                                                                                       SOFTWARE: FastSEQ
SEQ ID NO 5
LENGTH: 36778
                Query Match
Best Local Similarity
                                                                                                                                                                   TITLE OF INVENTION: DNA encoding methymycin FILE REFERENCE: 600.438US1 CURRENT APPLICATION NUMBER: US/09/860,846 CURRENT FILING DATE: 2001-05-18 PRIOR APPLICATION NUMBER: 09/105,537 PRIOR FILING DATE: 1998-06-26
 Matches
                                                             ORGANISM: Streptomyces -09-860-846-5
                                                                                                                                                    NUMBER OF SEC ID NOS:
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                                                                                           TYPE: DNA
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Sequence 5, Application US/09861289 Patent No. US20020110897A1
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GENERAL INFORMATION: APPLICANT: Sherman,

Sherman, D.H. Liu, H.

APPLICANT:

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LENGTH: 36778
TYPE: DNA
ORGANISM: Streptomyces
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CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
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SOFTWARE: FastSEQ for Windows Version
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Local Similarity 44.88;
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APPLICANT: Liu, H.
APPLICANT: Liu, Y.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
CURRENT APPLICATION: DNA encoding methymycin and FILE REFERENCE: 600.438US1
CURRENT FILING DATE: 2001-05-18
CURRENT FILING DATE: 2001-05-18
PRIOR ETLING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PastSEQ for Windows. Version 3.0
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LENGTH: 11220
TYPE: DNA
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; LENGTH: 11220
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US-09-861-289-32
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APPLICANT: Sherman, D.H.
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Best Local Similarity 45.7%;
Matches 332; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/861,289 CURRENT FILING DATE: 2001-05-18 PRIOR APPLICATION NUMBER: 09/105,537 PRIOR FILING DATE: 1998-06-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1
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                                                                             CTTCCGCATCGGCCGCGAGCTGGACGTGCCGGTGGTGATCTCGCACCACGAGGTCATGGG 800
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                                                                                                            CCTGGCGTTCGGCCCGACCATGATCGGCTCCGACGGCCTGCCGCACGACGACGACGCCCGCA 1160
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                                                                       CCGTCTCAACGCCGCGACCGGGCTGCGGCTGCCGGCCACGCTGGTCTTCGACCACCCCAC 10898
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Search completed: January 14, 2003, 08:03:19 Job time: 447 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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US-09-385-028-1
US-09-105-537-30
US-09-105-537-5
US-09-320-878-19
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0S-09-031-606-8

0S-09-031-606-10

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0S-08-458-537-1

0S-08-451-775-9

0S-08-461-775-11

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67.2	67.2	67.2	67.4	67.4	67.8	68	89	68.2	68.2	68.6	. 68.6	68.8	68.8	68.8	69.6	70	71.2
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Sequence 4,	Sequence 4,	Sequence 4,	Sequence 1,	Sequence 1,	Sequence 13,	Sequence 1,	Sequence 1,	Sequence 6,	Sequence 14,	Sequence 1,	Sequence 7,	Sequence 1,	Sequence 1,	Sequence 1,	Sequence 32,	Sequence 2,	Sequence 1,
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ALIGNMENTS

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US-07-945-283-1/c
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GENERAL INFORMATION:
APPLICANT: Cheung,
                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext
TELEFAX: 309-685-4128
INFORMATION FOR SEQ ID NO: 1;
                                                                                                               TOPOLOGY: line
MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wesley, TITLE OF INVENTION:
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pairs
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                  LOCATION: FEATURE:
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CITY: Peoria
STATE: IL
COUNTRY: USA
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                                                                                                  ORGANISM:
                                                                                                                                                                                              TYPE: NUCLEIC ACID
STRANDEDNESS: doub
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replace(1099, "g")
                   variation
                                                                                                    Pseudorabies virus
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Ronald D.
Pseudorabies Virus Deletion Mutants
Involving The EPO and LLT Genes
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Best Local Similarity 44.5%;
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LOCATION:
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      AATTTCGGCCGCTCGCGAGACGCTGCCGCTGATCGAGGCCGCCATGGCGCCAGGAC
                                G---GCCGCGAGCTGGACGTGCCGGTGGTGATCTCGCACCACAAGGTCATGGGCCCAGCCC
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pred. No. 8.8e-10;
0; Mismatches 738;
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; ORGANISM: Streptomyces venezuelae
US-09-105-537-7
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                                                                                                                                                                 Matches 439;
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Best Local :
                                                                                                                                                                                                                                                                                                                  APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
APPLICANT: Chao, L.
APPLICANT: Chao, L.
APPLICANT: Chao, L.
APPLICANT: Chao, L.
APPLICANT: Shao, L.
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
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                                                                                                                                                                           Match 4.78;
Local Similarity 44.28;
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                       CCATCGGCGATCTGTCGGACGCCGCCGCGCACACCCCGGGTCGACGTGTCGGGCCTGGTGG
                                                    TCACCCCGGTCTTCGCCGACATCGACCCGGGACACCGGCAACCTCGACCCGGACCAGGTGG
                                                                                                                                                                 Conservative
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Windows Version
                                                                                                                                                                 0; Mismatches 542;
                                                                                                                                                                              Score 81.8;
Pred. No. 1.
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APPLICANT: Liu, H.
                                                                                                                                                                     Sequence 3, Application US/09105537A Patent No. 6265202
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEO ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
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; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/773,816
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/243,458
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: US 60/179,305
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 23673
TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-RECEPTOR TITLE OF INVENTION: ANTAGONISTS FILE REFERENCE: 28600-20210.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stanford University APPLICANT: Khosla, Chaitan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(23623)
OTHER INFORMATION: n = A,T,C or G
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    8262
                                                                                                                                                              8382 GCCCTCGGGCAACTGGACGAGGCCGGCGTGTTGACCATCTCGCTGGTCACCGACCCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 GGCGTGCGCGGCGACCGCATCGCCGATCGGCGATCTGTCGGACGCCGCGCGCACACC 186
                                                                                                                                                                                                                                                                                                                                                           304 ACGGTGGTCACGGGCAATTGCGGCATCAGCCTGGCGCCGCTGGCGCACGCCAACCCCGCCC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                         247 GACAACTACCTGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCG---TCACC 303
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Local Similarity 42.4%;
hes 667; Conservative
                               544 GCCATGGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCGGCATTTCGACCGGC 603
                                                                                                                   484 ACGCTGCGCGCGCGGTCATGCCGGACTTGCAGCGCGCCGCCACCGACGAGGAAATCGCG 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCTCGACGAGGCCGTCGTCATCGTGACCGGCCGGATCCACGGCCAGCCGCTCGTCGTC 8563
                                                                                                                                                                                                   CTGGACGCGTTGCGGGCCACGCCGGCCGGCCGTCAACGCCGCCTGTATGGTGGGCCCATTCA 483
                                                                                                                                                                                                                                            GGCGGCGCGCATGCAGGAAGGCGCCGTCGCGCTCATGCAGATGGCCAAGACCAGCGCC 8383
                                                                                                                                                                                                                                                                                                                         ACCCTCGCCGAGACCGCGCTCGCCGAACACCTGCCGCTGCTGATCGTCAGCGCGTCC 8443
                                                                                                                                                                                                                                                                                                                                                                                                     GCCGCGATGGACTTCGCGTTCCTCGGCGGCGGCAGCCTGGGCGGCGGTCGGCGAACTGATC 8503
TACGGCGGCGTCGTTCGCGACCCTGTGCGACGTCATCGTCGCCGAACCCCGGC 8263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 77.4; DB 4; Length 23673; Pred. No. 1.5e-06; 0; Mismatches 891; Indels 15; Gaps
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	18 GAAGTGATGGGCG 1630	16	gg
		71	VQ
1617 7189	58 AACCGCTACATGGCCCCTCCCCTCCGCTAGATACGGCCCACCGATATCGTGGGCAAG	15 72	ру
1557	B CAGCCCTTACAATCCGGCGTGAACGGGGCGGCGTGCCGCCCCCCCC	1498	d
7249		7308	V
1497		1438	DB
7309		7368	DB
1437	B GACCGCCCCCCGCATCCATTCCGTGTACGTCAACGGCGCGCCGGTCTGGCAAGAGCAG	1378	Оу
7369		7428	Об
1377	B GACCTGGTGGTGTTCGACCCGGCCACCGTGGCCGATACCGCCACCTTCGAACACCCTACC	1318	g
7429		7488	82
1317	ACCGCCGCGCGCTTCGGCCTGGCCGGGCGGGGCAGCTGCAGGCCGGGTACTTCGCC	1261	dp
7489		7548	Qy
1260	TATECGCGCGACCTGGGCCTGTTCCCGCTGGAGACGGCGGTATGGAAGATGACCGGCCTG	1201	ду
7549		7608	Ду
1200 7609	CCCCACGACGACCCCCCCATCCCCCCCTGTGGGGCACCTTCCCGCGGGTGCTGGGGCACCCCCCGCGGGGCCCACCCTGCCGAGAACCTGCGCCTGCCCAGGGCCAGGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGAGAACCTGCGCCTGCCAGGCCAGGAACCTGCGCCTGCCAGGAACCTGCGCCTGCCAGGAACCTGCCCTGCCGAGAACCTGCGCCTGCCAGGAACCTGCGCCTGCCAGGAACCTGCGCCTGCCT	1141 7668	Qу
1140 7669	GAACCCGACGTGCAGCGCATCCTGGCGTTCGGCCCATCATGATCGGCTCCGACGGCCTG	1081 7728	P Q
1080	TCCAAGTACGACGTGGTGCCCGAGCTGCAGCCGGCCGGCC	1021	д
7729		7782	У
1020	AAGCCCTTCCCCGAACTGAGCGGGCGGCCGACCTGGATGAAGTCGCCGCCGAGCGCGGCAAA	961	g
7783		7842	9
960	TCCACCATGCTCAAGCAGGACCGCTGCTGCTGCCGGCCGG	901	B
7843		7902	64
900	ATCGAGGCGCCATGGCGCGCAGGACGTCTCGCTGGACGCGTATCCCTACGTGGCCGGC	841	g
7903		7962	Qy
840 7963	TCGCACCACAAGGTCATGGGCCAGCCCAATTTCGGCCGCTGGCGGGAGACGCTGCCGCTG	781 8022	Db Qy
780 8023	CCCCCCTGGAGGAAACCTTCCCCATCGCCCGAGCTGGACGTGCCGGTGGTGATCGCCGTACGTCGCCGGAGCGGGCATCCCCGTACGTCGCCGGGGGAACCGGCAACCGCCGACGCCGCGGCATCCCCCGTACGTCGCCGGAGGGAACCGGCAACGCCGGAGGCATCCCCGTACGTC	724 8082	90
723 3083	CTGAGCGCGCATGGCGGCATCTACGCCCACATGGGCGACGAAGGCGAĞCACATCGTG 7	664 8142	8 5
8143	GCCTTCTACCCGCCGCCGCCGCCGCCGCCGCCGAGAGATCATCGAGGTGTGCCGGCCG	604 8202	8 8

US-09-320-878-21/c

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; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-21
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SOFTWARE: PatentIn Ver. :
SEQ ID NO 21
LENGTH: 5970
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Best Local Similarity
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EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER FILING DATE: 1998-09-22.
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER APPLICATION NUMBER: 60/087,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: CIP OF 09/141,908 EARLIER FILING DATE: 1998-08-28
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APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: CIP EARLIER FILING DATE: 1998-05-06
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APPLICANT: TANG, Li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661 TCACCCCGGTCTTCGCCGACATCGACCCGGACACCCTCGACCCGGACCAGGTGG 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 CCATCGGCGATCTGTCGGACGCCGCGCGCACACCCGGGTCGACGTGTCGGGCCTGGTGG 211
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                                                                                                                                                                                                                                                                                                               541 GCGCCGCCGACCAGCTGCGGAAGGTCGCCGACGACGACGCCTGCGGCTGTACTTCGACG
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                                                                                                                                                                                      GCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGGGCCACGCCGGCGG
                                                                                                                                                                                                                                                                        GCCTGGCGCCGCTGGCGCCAACCCCGCCCGCCCCTGGACCTGCTGGACGAAGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334;
TGCAGCGCCGCCACCGACGAGGAAATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCA 571
                                                                   TCACCGACGACGCCGACCTCGCCGCCCGGATCCGCCCCTCCACAACTTCGGCTTCGACC 305
                                                                                                     CCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCGCCGCGGTCATGCCGGACT
                                                                                                                                                 AGGTCTTCAGCTTC----CACGCCACCAAGGCCGTCAACGCCTTCGAGGGCGGCGCCGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21, Application US/09320878A
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Pred. No. 2.2e-06;
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US-08-804-227C-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           TELEPHONE: 317-276-24
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/804,227C FILING DATE: February 21, 1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 TGCCCGGCGCAGCCCCGCCGGCGGACCAACGCCAAGATGAGCGAGGCCGCCGCCGCCA
                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     692 CCCACATGCGCGACGAAGGCGAGCACATCGTGGCCGCGCTGGAGGAAACCTTCCGCATCG
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                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             632 CCACCGAAGAGATCATCGAGGTGTGCCGGCCGCTGAGCGCGCATGGCGGCATCTACGCCA 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 TGGGCCTCACCTCCCTCGACGCGTTTCCCGAGGTCATCGACCGGAACCGGCGCAACCACG 185
                                                                                           FEATURE:
                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 ACGGCCTCAACAACCACCAGTACGTGATCGTCGAGATCGACGAGGCCACCACCGGCATCC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 CCGSCTACCGCGAGCACCTCGCGGACCTCCCCGGCGTCCTCGTCGCCGACCACGACCGCC 125
                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: INDIANAPOLIS
                                                                                                                                                                                                                                    STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                      NAME/KEY:
 LOCATION:
                   NAME/KEY:
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14351..19945
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816..14234
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20010..31199
31232..36067
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NAME/KEY:

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US-08-804-227C-1
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                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08461775 Patent No. 5858773
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: MAZODIER, Philip
APPLICANT: GUGLIEMI, Gerard
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                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                  CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                 George Mason Bldg.,
                                                                                                                                                                                                                                                             MAZODIER, Philippe
                                                                                                                                                   Burns, Doane, Swecker & Mathis orge Mason Bldg., Washington &
                                                                                                                                                                                                                 REGULATORY INITIATION
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        Version #1.25
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CURRENT APPLICATION DATA:

US/08/461,775

APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 43

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                                       RESULT 8
US-09-031-606-8
Sequence 8, Application US/09031606 Patent No. 6153404
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NFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
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APPLICATION NUMBER: FR 9011186
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TOPOLOGY: lin
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                                                                                                                           CATGGCCTTCGACAAGGGC
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Pred. No. 3.2e-06;
0; Mismatches 265
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Best Local Similarity 46.9
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PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/050,31
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 836-20 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
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REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010
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GCTCGACACCGCGCGCCCGATCGACGACGACGACGACATCGCCGCCGCCGTCGCCGCCGCTCTC
                                                                        CTCCCCGGCCGCCTGAAGAAGGGCATCGACGCCGCCGTCGCCGCCGTCTCCGCCGAGCT 389
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Pred. No. 3.2e-06;
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US-08-461-775-10
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                                                                           Query Match
Best Local
                                                           Matches
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                                                                                                                                                                                                                                                                         TELEFAX: (703) 836-20: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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LENGTH: 1620 base pair
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CITY: Alexandria
                            297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                NAME: Crane-Feury, Sharon E REGISTRATION NUMBER: 36,113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
 90
                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 010830-035
                                                                         Local Similarity
                                                                                                                                      LOCATION:
                                                                                                                                                    NAME/KEY:
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TOPOLOGY: li
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                            CGTCACCACGGTGGTCACGGGCAATTGCGGCGATCAGCCTGGCGCCGCTGGCGCACGCCAA 356
 CGGCCCCAAGGCCGCAACGTCGTCATCGACAAGAAGTTCGGCGCCCCGACCATCACCAA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RY: United States 22313-1404
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                                                           Conservative
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                                                            0;
                                                           Score 75; DB 2;
Pred. No. 3.3e-06;
0; Mismatches 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10,
                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 10-MAY-19
APPLICATION NUMBER: FR
FILING DATE: 10-SEP-19
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GUGLIEMI, TITLE OF INVENTION: F
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 CGACGGCGTCACCATCGCCCGTGAGGTCGACGACGACCCCGTACGAGAACCTCGGCGC
                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         570 CATGGCCTTCGACAAGGGC 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          717 CATCGTGGCCGCGCTGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGTGCCGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 GCTCGACACCGCGCGCCCGATCGACGACAAGTCCGACATCGCCGCCGTCGCCGCGCTCTC
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                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Alexandria
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                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                             REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAZODIER, Philippe
                      (703) 836-2021
                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burns, Doane,
                                                                                                                                                           10-SEP-1990
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INITIATION
                                                                                                                                                                        FR 9011186
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Best Local Similarity 46.9%;
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08458568A Patent No. 5821339
GENERAL INFORMATION:
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                                                                                                                                                                                                                                               TITLE OF INVENTION: Composition TITLE OF INVENTION: Infections NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schaffer, Priscilla A. APPLICANT: Yeh, Lily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597
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                                                                                                                                                                          STREET: One Liver CITY: Philadelphia
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                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
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                                                                                                                            COUNTRY: U
                                                                                                                                                                                                         ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCGCCCGCCCCTGGACCTGCTGGACGAAGGCGCTCTTACCGTTTCGAGCGCTTCGC 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGACTACCTGGACGCGTTGCGGGGCCACGCCGGCGGCCGTCAACGCCGCCTGTATGGTGGG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATCGCGGCCATGCGGGACCTGGCCGAGGGGAAGCCATGGCCAAGCGGCCACGGCGCCATTTC 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATCTCGCACCACAAGGTC 795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACCGGCGCCTTCTACCCGCCCGCCGCCGCCGCCACCGAAGAGAGATCATCGAGGTGTG 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCGACCGTGCTGGCCCAGGCGCTGGTCCGCGAGGGCCTGCGCAACGTCGCCGCCGGCGC
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APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                    Compositions and Methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 75; DB 3;
Pred. No. 3.3e-06;
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                                                                                                                                                                                                                                                                                                                  Treatment of Herpesvirus
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rocal Similarity
ronser
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: LEATY Ph.D., Kathryn
REGISTRATION UMBER: 36,31:
REFERENCE/DOCKET NUMBER: DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5065
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                                                                                                                                                                                                                      ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Herpes simplex virus TSTRAIN: Herpes Simplex Virus T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                CCTGGACCTGCTGGACGAAGGCGGCTCTTACCGTTTCGAGCGCCTTCGCCGACTACCTGGA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCACGGGCAATTGCGGCATCAGCCTGGCGCCCCACGCCAACCCGCCCCGCCCC 368
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CACCACAAGGTCATGGGCCAGCCCAATTTCGGCCGCTCGCGCGAGACGCTGCCGCTGATC
                                                                                                                        CTGAGCGCGCATGGCGCATCTACGCCACCCACATGCGCGACGAAGGCGAGCACATCGTG
                                                                                                                                                                                       GCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCC----ATCGGCATTTCGACCGGC
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                                                                                                                                                                                                                                                                                                                                                                              CGCGTTGCGGGCCACGCCGGCGGCCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCT 488
                                                                                                                                                                                                                                                                                                                                                                                                             CCGATACGACCGCGCGCAGAAGGGCTTCCTGCTGACCAGCCTGCGCCCGCGCCTACGCGCC.
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                                                                                                                                                       GCCGCGCTGGAAGCCTTCCGCATCGGCCGCGAGCTGGACGTGCCGGTGGTGATCTCG
                                                                                            CGCCGCGCCCAGGCCGGCCGTGGCCGTCGAGTGCCTGGCCGCCTGCCGCGGGATCCTG
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Pred. No. 5.2e-06;
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Query Match

4.2%; Score 73.8; DB

Best Local Similarity 43.2%; Pred. No. 7e-06;

DB 4;

Length 15872;

4;

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FILE CANT: Zhao, L.
FITTLE OF INVENTION: DNA encoding methymycin and
FILE REFERENCE: 600. 438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 15872
TYPE: DNA
ORCANTER
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Patent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
ORGANISM: Streptomyces -09-105-537-1
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                                                ; MOLECULE TYPE: US-08-461-775-9
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US-08-461-775-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Appli
Patent No. 585877
Query Match
Best Local Similarity
                                                                                                                                 TELEFAX: (703) 836-202:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION: (703) 836-6620
                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Alexandria
                                                                             TOPOLOGY:
                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                     H: 2167 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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, 836-2021
, NO: 9:
                                                           (genomic)
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4.2%;
46.7%;
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Score 73.4; DB 2;
Pred. No. 6.8e-06;
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US-09-031-606-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                     PRIOR APPLICATION DATA:
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                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: REGULATORY TITLE OF INVENTION: INITIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MAZODIER, APPLICANT: GUGLIEMI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1238 GCTCGACACCGCGCGCCCGATCGACGACAAGTCCGACATCGCCGCCGCTCGCCGCGCTCTC
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                                                                    FILING DATE: 10-MAY APPLICATION NUMBER:
                                                                             IOR APPLICATION NUMBER: US UNAPPLICATION NUMBER: US UNAPPLICATE: 10-MAY-1993
                                                                                                                                           CLASSIFICATION:
                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                   CITY: Alexandria
STATE: Virginia
COUNTRY: United States
                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                        ZIP: 22313-1404
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                                                                                                                                                                             APPLICATION NUMBER:
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Crane-Feury, Sharon E
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George Mason
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAZODIER, Philippe
                                                   UMBER: FR 9011186
10-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerard
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                                                                                                       US 08/050,313
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g., Washington
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US-08-461-775-11
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Patent No. 5858773
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 2167 base pairs
                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                           APPLICANT: MAZODIER, Philippe APPLICANT: GUGLIEMI, Gerard
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                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                          TITLE OF INVENTION:
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hes 233; Conserv
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                                                                  CITY: Alexandria
STATE: Virginia
                                 COUNTRY: United
ZIP: 22313-1404
                                                                                                       STREET:
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Pred. No. 6.8e-06;
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Search completed: January 14, 2003, 06:36:00 Job time : 334 secs
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1118
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STRANDEDNESS: single
TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: 010830-035
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Match
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AT TONMENTS		AG032979	BM458211	AG128373	AG039543	AG077581	AG065058	BG786331	AG049208	BG607300	BG809816	AG060116	AG030608	AG162326	AG039481	AG075424	AG043615	AG072425	BG852371	AW731151	AW731212	BQ687717	CNS0072Q	BM810045	CNS006XK	BM926731	BM463178	AG043477	AG042920	CNS006XK	BQ678719	BG852363	AG127788	AG030607	AG076818	CNS0091P	AG030611	CNS0072Q	AG039481	CNS0091P
-	-	G032979 Par	58211 AGE	128373 Par	039543 Par	7581	065058 Par	786331 SEA	49208 Pan trog	7300 WHE2493_	09816 mgct001x	60116 Pan	030608 Pan troq	162326 Pan trog	9481 Pan trog	075424 Pan trog	43615 Pan trog	72425 Pan	52371 102	31151 GA_	212	87717	66742	1004	66051	26731	463178	04347	2920	20	8719 AGE	2363 102	7788 E	030607 Pan	076818 Pan	053013 Drosophi)30611 Pan troq	066742 Dr	9481 Pan troq	053013 Drosophi

ALIGNMENTS

	source	FEATURES								COMMENT	JOURNAL		TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BG809984
/organism="Magnaporthe grisea" - /strain="70-15"	11516	Location/Qualifiers	Seq primer: T3 primer (AATTAACCCTCACTAAAGGG).	Email: ralph_dean@ncsu.edu	Fax: 919-513-0024	Tel: 919-513-0020	Campus Box 7251, Raleigh, NC 27695, USA	North Carolina State University	Fungal Genomics Laboratory	Contact: Ralph A. Dean	Unpublished (2001)	library in the rice blast fungus, Magnaporthe grisea	Construction and sequence analysis of an appressorium stage cDNA	Choi, W. and Dean, R.A.	1 (bases 1 to 1516)	Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.	<pre>Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;</pre>	Magnaporthe grisea	Magnaporthe grisea.	EST.	BG809984.1 GI:14180964	BG809984	grisea cDNA clone mgct002xd11f 5', mRNA sequence.	mgct002xd11f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe	BG809984 1516 bp mRNA linear EST 22-MAY-2001	

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BASE COUNT
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CTACGTGGCCGGCTCCACCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCAT
                                    GACGCTGCCGCTGATCGAGGCCGCCATGGCGCCCAGGACGTCTCGCTGGACGCGTATCC
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a 657 c 660 g 16 t 118 others
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/clone="mgct002xd11f"
/clone_lib="Magnaporthe grisea Appressorium Stage cDNA"
/dev_stage="Germinated conidia on apprressorium-inductive
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AG171124
AG171124.1
                                                                                                                                                                                                                                                                                                          (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Fujiyama, The Institute of Fujiyama and Chemical Research (RIKN), Genomic Sciences Center (GSC); and Chemical Research (RIKN), Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, Kanagawa 240-0045, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AG171124 1798 bp DNA linear Pan troglodytes DNA, clone: RP43-040F09.TJ, genomic
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Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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Totoki,Y., Watanabe,H.
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                                                                                                                                                                                                                            LIBRARY
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R.Site 2
                                                                                                                                                                                          Vector
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/db_xref="taxon:9598"
                              /organism="Pan troglodytes"
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                                                                                                                      : pBACe3.6
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/sex="male"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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Pan troglodytes
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Primates;
                                                                                  AG171124.1 GI:16700802
AG171124.1 GI:16700802
GSS.
Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-040F09.TJ.
                Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D. Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library RPCI-43
        Unpublished
                                                                                                                                                       Pan troglodytes DNA, clone:
                                                                                                                                                                 AG171124
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                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
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AUTHORS TITLE

Fujiyama, A., Hattori, M., Totoki, Y., Watanabe, H. an Direct Submission

and Sakaki, Y.

Yada, T.,

(bases 1 to 1798)

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CCGACGAGGAAATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGG--CGC
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Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones RPCI-43 This BAC Clones RPCI-45 
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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/db_xref="taxon:9598"
/clone="RP43-040F09.TJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japa
                                      Totoki,Y., Watanabe,H. Direct Submission
                                                              Fujiyama,A.,
                                                                                                                            Fujiyama,A.,
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                Pan
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                                                                                                     BAC end
                                                                                                                   Totoki,Y., Watanabe,H.
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                                                                                                                                                                                                                                                          Pan troglodytes DNA, clone:
                                                                                                                                                                                                                                                                       AG032943
                                                                             (bases 1 to 1542)
                                                                                                                                                                                           troglodytes male lymphoblast DNA, Library clone:PTB-007N10.F.
                                                                                                                                                                                troglodytes
                                                                                                    sequences of Library PTB
                                                  Hattori,M., Toyoda,A., atanabe,H. and Sakaki,Y.
                                                                                                                             Hattori, M.,
                                                                                                                   and
                                                                                                                 Toyoda, A.,
nd Sakaki, Y
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                                                                Taylor, T.D.,
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                                                                Yada, T.,
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                                         GCGCGCATGGCGGCATCTACGCCACCCACATGCGCGACGAAGGCGAGCACATCGTGGCCG
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                                                                                                                                               TGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCGGCATTTCGACCGGCGCCT 607
                                                                                                                                                                                                                                                                                                                                        (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY
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/clone_lib="PTB Chimpanzee Male
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/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pan troglodytes"
/db_xref="taxon:9598"
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CCGCGCTGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGTGCCGGTGGTGATCTCGC
                                 TGAGCGCGCATGGCGCATCTACGCCCACCCACATGCGCGACGAAGGCGAGCACATCGTGG
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                                                                                                                                                                                                                                           ACAAGGTCATGGGCCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgplgsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiyama, A., Hattori, M. Totoki, Y., Watanabe, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/clone_lib="PTB Chimpanzee Male BAC Library"
488 c 540 g 24 t 120 others
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/sex="male"
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/db_xref="taxon:9598"
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PTB-003A18.R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Construction and sequence library in the rice blast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choi, W. and Dean, R.A.
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    Location/Qualifiers
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/dev_stage="Germinated conidia
surface"
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   542
                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library
GSTTBGSTTTTTTSSGSGYGKGCSSGSGBSCSCCSSCSSCSSCSCCBCCCCCSCSSYCC 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea: Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNSU091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope.
Direct Submission
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                                                                                                                                                                                                                                                                                                                    /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/db_cxref="taxon:7227"
/clone="Back19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
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                                                                                                                                                                                       4.1%;
                                                                                                                                                Score 72.4; DB 17;
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90; Mismatches 143;
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JOURNAL REFERENCE
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                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                            clone tracking errors.
                                                                                                                                                                                                                                                                                                                             vas generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAC end sequences of Library PTB
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                             LIBRARY
                                                                                                                                                                                                                                                                                                PRIMERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           troglodytes male lymphoblast DNA, Library clone:PTB-016J15.F.
                                                                                                                                                                                                       Vector
R.Site 1
R.Site 2
                                                      24
                                                                                                                                                                                                                                                                          Sequencing: -21M13
                                             /Clone_lib="PTB Chimpanzee Male BAC Library" 571 c 592 g 31 t 81 others
                                                                                                                                                                                         Location/Qualifiers
                                                                                                    /clone="PTB-016J15.F"
/sex="male"
                                                                                 /cell_type="lymphoblast"
                                                                                                                                        /db_xref="taxon:9598"
                                                                                                                                                       /organism="Pan troglodytes"
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PTB-016J15.F,
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Matches Best Local

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CGCGCCCGGCTTCATCGACTCGCACACCCACGACGACAACTACCTGCTCAGGCGTCGCGA
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
                                                                                              AL066742.1 GI:4945205
                                                                                                               fly), genomic survey sequence. AL066742
                                                         melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGCTGGAGACGGCGTATGGAAGATGACCGGCCTGACCGCCGCGCGCTTCGGCCTGGCC
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fi
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    Web : www.genoscope.cns.fr)

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Pan troglodytes DNA,
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a 202 c 241 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (E-mail:chimpbes@gsc_riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiyama.A., Hattori,M., Toyoda,A., Taylor,T.D., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/db_xref="taxon:9598"
/clone="PTB-003A20.F"
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/clone_lib="PTB Chimpanzee Male
476 c 700 g 14 t ]
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RESULT 11
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Best Local :
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1254 CGGCCTGACCGCCGCGCTTCGGCCTGGCCGGGCGGGCAGCTGCAGGCCGGGTACTT 1313
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                                                           SSGTSSACVKCNASSSCGCCGCGMABCCMCSSSSSCCGSASARGVKVRASGGAGKRGGGS
                                                                                              GGGGCACTATGCGCGCGACCTGGGCCCTGTTCCCCGCTGGAGACGGCGGTATGGAAGATGAC 1253
                                                                                                                                       CSBSCSCSCSCSSBSCSSSSMSTSSSNSSBCSSCSSSBSSSSTSSMSSSSBSSSSGSSSS 866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw Sp, the same strain used for the BDGP's Pland EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insc
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.f. Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS0091P
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AL053013.1 GI:4934461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found at http://bacpac.med.buffalo.edu/drosophila_bac.htm
                                                                                                                                                                                                                                     Similarity
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/db_xref="taxon:7227"
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/note="end : TET3"
61 c 61 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes DNA, clone: PTB-071C05.R, genomic survey AG076818
                                                                                                                                                                                                                                                                                                                                                               Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                    clone
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R.Site 2
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                                                                                                                           /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
488 c 514 g 23 t
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/db_xref="taxon:9598"
/clone="PTB-071C05.R"
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Pan troglodytes DNA, clone: PTB-003A18.F, genomic survey sequence. AG030607.1 GI:16557480
GSS.
Submitted (02-AUG-2001) Asao Pujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@ggc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                              Pan
BAC
                                                                                                                         Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                      Unpublished
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                            Direct Submission
                                                                                                                                                                                       BAC end sequences of Library PTB
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Sutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                         Taylor, T.D.,
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                                                                   GCTTCGGCCTGGCCGGGCGCGGCAGCTGCAGGCCGGGTACTTCGCCGACCTGGTGGTGT
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GCCGCCGCGCGCCNGCCCGCCCCNCNNCGCGCGCGGNNCNCNCGCGGGCNGCCCGNNCG
                                                                                            ACCNCGGGCGCGCGCGCGCGCGCGCGNNCGNNCGCGCGCCNCGGCGCGCCNCCGCGG
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/clone_lib="PTB Chimpanzee Male
669 c 552 g 64 t 1
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/db_xref="taxon:9598"
/clone="PTB-003A18.F"
/sex="male"
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Pan troglodytes DNA, clone: PTB-138MO2.R, genomic
AG127788.1 GI:16656953
                                                                                                                                                                                                                                                                                                                                                   (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC was generated during the R&D process and may have higher chance
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Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                       clone tracking errors.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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BAC end sequences of Library PTB
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Totoki,Y., Watanabe,H. and Sakaki,Y
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
                    Similarity
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                                                                                                                                                                                                                                                                          Vector
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                                                                                /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
369 c 480 g 44 t 1
                                                                                                                                                    /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-138M02.R"
                                                                                                                                       /sex="male"
                                                                                                                                                                                                      Cocation/Qualifiers
                   4.0%;
                                                                                                                                                                                                                                                         : pKS145
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 Score 71; DB Pred. No. 0.03 0; Mismatches
                   DB 17;
0.03;
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GCGCGAGACGCTGCCGCTGATCGAGGCCGCCATGGCGCCGCCAGGACGTCTCGCTGGACGC 881

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RESULT 15
BG852363
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              KEYWORDS
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                                      ACCESSION
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Chlamydomonas reinhardtii.
                          BG852363
BG852363.1 GI:14233547
                                               1024034A03.y2
Chlamydomonas
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                                                 1281 bp mRN
C. reinhardtii CC-1690,
reinhardtii cDNA, mRNA s
                                                  mRNA sequence.
                                                                       mRNA
                                                           normalized,
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                                                                                                                                                    Grossman,A., Davies,J., Federspiel,N., Harris,E., McDermott,J.P., Silflow,C., Stern,D. and Surzycki. Analyses of the Chlamydomonas reinhardti Genome: Unicellular System for Analyzing Gene Function and Vascular Plants; project phase 2
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Durham, NC 27708-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 919 613 8159
Fax: 919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with Exassist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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                                                                                                                      1056 CGGCGCCATCTACTTCATGATGGACGAACCCGACGTGCAGCGCATCCTGGCGTTCGGCCC 1115
                                                                                                                                                                                                                                               876 GGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACCGCGTGCTGCTGGC 935
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Search completed: January 14, 2003, 08:47:43 Job time: 2627 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                           Score
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Gapop 10.0 , Gapext 1.0
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
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AAD17184
AAD17186
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                                                                    Alcaligenes xyloso
DNA encoding an am
Human adenosine Al
Human ORFX polynuc
Streptomyces nours
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             Streptomyces nours
DNA encoding Pseud
Human adenosine Al
Streptomyces nours
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AAC91797
ID AAC9
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AC AAC9
AAC91797;
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	207707	ا د	12975	٠ ا ١	ِ د	44	
Pseudomonas aerugi	AAS51474	2	18	4.1	2	4 ω	
Streptomyces clavu	AAD14499	22	15079	4.1	'n	42	
S. clavuligerus cl	AAQ91580	16	15079	4.1		41	
Streptomyces clavu	AAD14501	22	11604	4.1	2	40	
Human METH1 relate	AAZ32022	20	5224	4.2	73.2	39	
L05390 cDNA clone.	AAC90079	22	5224	4.2	ω	38	
Infected cell prot	AAV10362	19	4257	4.2	w	37	
ro -	AAV68520	19	4257	4.2	73.4	36	
٠.	AAZ87283	21	15872	4.2	ω.	35	•
omýces ven	AAT68715	18	15872	4.2	w.	34	
Q	AAQ22485	13	2668	4.3	75	ω	
gro es el operon w	AAQ22484	13	2167	4.3	75	32	
groEL-1 gene codin	AAQ22482	13	1620	4.3	75	31	
Sequence encoding	AAN92408	10	2061	٠.3	5	30	
Tylactone synthase	AAT80413	18	43280		75.6	29	
Orf virus genomic	AAT91361	18	4020	٠	5	28	a
Nucleotide sequenc	AAA58471	21	58857	4.3	7	27	
ngium cellu	AAT06769	17	28598		. 76	26	
HSV L/ST region.	AA076213	16	12001	٠		25	C
	AAZ56003	21	5970		6.	24	O
	AAA75635	21	5970	4.3	76.2	23	O
	AAD25519	24	154746	4.4	8	22	C
Human herpesvirus	AAD25519	24	154746	4.4	8	21	
Complete nucleotid	AAC55857	21	833	4.4	8	20	
te Mitomy	AAC55840	21	12249	4.4	8	19.	
immediate e	AAA09686	22	3957	4.4	8	18	
	AAQ22481	13	1320	4.5	9.	17	
treptomyces	AAD39043	24	361	4.7	۳.	16	O
. venezuelae	AAZ87319	21	13613	4.7	۳.	15	O
venezuela	AAZ87284	21	12441	4.7	۲.	14	O
н	AAD39044	24	1248	4.7	Ϊ.	13	
	AAZ87286	21	1248	4.7	ŗ	12	
	98	22	109519	4.8	84.6	11	
88421nt genomic DN	AAL40781	24	842	4.9		10	

ALIGNMENTS

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D-aminoacylase; zinc tolerant host; recombinant production; zinc-enhanced expression; D-form amino acid synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alcaligenes xylosoxidans subspecies xylosoxidans D-aminoacylase DNA
WPI; 2001-080828/09.
P-PSDB; AAB48975.
                                                                      Takeuchi K, Koide Y,
                                                                                                                                                                     17-JUN-1999;
                                                                                                                                                                                                             15-JUN-2000; 2000WO-JP03932
                                                                                                                                                                                                                                                                                                            WO200078926-A1
                                                                                                                                                                                                                                                                                                                                                          Alcaligenes xylosoxidans.
                                                                                                                                                                                                                                                                                                                                                                                                                                antibiotic production; peptide drug; pharmaceutical manufacturing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-2001
                                                                                                                                                                                                                                                                  28-DEC-2000.
                                                                                                                   (AMAN-) AMANO ENZYME INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                  99JP-0170555
                                                                        Hirose Y,
                                                                      Moriguchi M,
                                                                      Isobe
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The invention relates to a recombinant zinc-tolerant microorganism which expresses the D-aminoacylase from Alcaligenes xylosoxidans subspecies xylosoxidans. The presence of zinc ions in the culture medium enhances expression of the D-aminoacylase gene, and the invention also relates to the process of recombinantly producing the D-aminoacylase using the microorganism of the invention. The recombinant microorganism is used for the selective production of D-aminoacylase, which is useful in the synthesis of high optical-purity D-form amino acids for use in the production of antibiotics and peptide drugs. The present sequence represents DNA encoding D-aminoacylase from Alcaligenes xylosoxidans
                                                                                                                                                                                                                                                                                                                                                                                                                                  Transformed microorganism from zinc-tolerant host for selective production of D-aminoacylase, useful in synthesis of high optical-purity D-amino-acids for antibiotic side-chains and peptide drugs -
Sequence 1758 BP; 281 A; 662 C; 568 G; 247 T; 0 other;
                                                     subspecies xylosoxidans.
                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 14-18; 22pp; Japanese.
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                              GECGCCTTCTACCCGCCGCCGCCGCCGCCCACCACCGAAGAGATCATCGAGGTGTGCCGG
                                                        GGCGCCTTCTACCCGCCCGCCCGCCCGCCCACCAACAGAGATCATCGAGGTGTGCCGG
                                                                                  GCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGATCGGCATTTCGACC
                                                                                                         GCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCCATCGGCATTTCGACC 600
                                                                                                                                   CCGCTGAGCGCGCATGGCGGCATCTACGCCACCCACATGCGCGACGAAGGCGAGCACATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1758; DB 22; Length 1758; 100.0%; Pred. No. 5.8e-267; tive 0; Mismatches 0; Indels 0;
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720

	CTGAGCTACGAGAAGCTT 1758 	1741 1741	Фр
GATCGCC 1740 GATCGCC 1740	TCGCAGGCCAGCGGCATCGCGGTCTCGACCCTGTCCAAGGCCGAGCTGGGCCAG 	1681 1681	pb .
AGACCTG 1680 AGACCTG 1680	GTGATGGGCGCGCCCTGCGCGCCGAGCGCAAAGGCCCGGAAAATGACCCTGCAA 	1621 ·1621	Qy Db
CAAGGAA 1620 CAAGGAA 1620	CGCTACATGGCCCCTCCCTCCGCTCGCAATACGGCCCCACCGATATCGTGGGC	1561 1561	Db Qy
CGCAAAC 1560 CGCAAAC 1560	CCCTTACAATCCGGCGTGAACGGGGCGGCGTGCCGCCCCTCCCAACCCTGGAC 	1501 1501	Db dy
GCGCCAG 1500 GCGCCAG 1500	TTCACCGGCCAGCATGCCGGCCGCGCGTGCTCGCACGCAC	1441 1441	D Qy
GCAGGCG 1440 GCAGGCG 1440	CGCGCCGCCGGCATCCATTCCGTGTACGTCAACGGCGCGGCGGTCTGGCAAGAG 	1381 1381	Оу
TACCGAG 1380 TACCGAG 1380	CTGGTGGTGTTCGACCCGGCCACGGTGGCCGATACCGCCACCTTCGAACACCCT 	1321 1321	Qу
CGCCGAC 1320 CGCCGAC 1320	ACCGCCGCGCGCTTCGGCCTGGCCGGGCGCGGGCAGCTGCAGGCCGGGTACTTC	1261. 1261	Qу
CGGCCTG 1260 CGGCCTG 1260	TATGCGCGCGACCTGGGCCTGTTCCCGCTGGAGACGGCGGTATGGAAGATGACC 	1201 1201	Qу Db
GGGGCAC 1200 GGGCAC 1200	CCGCACGACGAGCGCCCGCATCCGCGCCTGTGGGGCACCTTCCCGCGGGTGCTG 	1141 1141	Qу Дъ
CGGCCTG 1140	AACCCGACGTGCAGCGCATCCTGGCGTTCGGCCCGACCATGATCGGCTCCGAC 	1081 G	Оу
SATGGAC 1080 SATGGAC 1080	CCAAGTACGACGTGGTGGCCGAGCTGCAGCCGGCGGCGGCGCCATCTACTTCATG 	1021 T 	Qу
CGGCAAA 1020 CGGCAAA 1020	AGCCCTTCCCCGAACTGAGCGGGCGCGACCTGGATGAAGTCGCGGCCGAGCGC 	961 A 961 A	рь
CTGGTGC 960	CCACCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCATCATCACC	901 T 901 T	dg VQ
3GCCGGC 900	TCGAGGCCGCCATGGCGCGCCAGGACGTCTCGCTGGACGCGTATCCCTACGTG	841 A . 841 A	ф
CCGCTG 840	CGCACCACAAGGTCATGGGCCAGCCCAATTTCGGCCGCTCGCGCGCAGACGCTG(781 T 781 T	Qу
GTGATC 780 GTGATC 780	TGGCCGCGCTGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGTGCCGGTGC 	721 G 721 G 721 G	Qу

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RESULT 2
AAA15140
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Best Local
                                                                                                                                              Matches
                                                                                                                                                                                                     rme present sequence encodes an aminocyclase enzyme. The enzyme is capable of hydrolysing N-acetyl-D-tryptophan at a substrate concentration of 10 grams per litre, and exhibiting faster conversed for N-acetyl-2-thlenylalanine than of R-N-acetyl-4-chlorophenylalanine. The enzyme can be used for the preparation of a D-amino acid by conversion of a corresponding D-N-acylamino acid. It can also be used for resolving a racemic mixture of N-acylamino acids and deprotecting optically-enriched N-acylamino acids. The D-amino acids are useful as intermediates the production of various pesticides, antibiotics and other pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                              New isolated D-amino acylase enzyme, useful for the preparation D-amino acids for use as intermediates in the preparation of pesticides, antibiotics and other pharmaceuticals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-1998;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-1999;
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                              GAGACGGCGGTATGGAAGATGACCGGCCTGACCGCCGCGCGCTTCGGCCTGGGCCGGGCGC
                                                                                                         GGCCCGACCATGATCGGCTCCGACGGCCTGCCGCACGACGACGCCCCGCATCCGCGCCTG
                                                                                                                                                                                                                                                                                   TCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACCGCGTGCTG
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AAX53491/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1264
             non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences ANX55272-74. These multiple target oligonucleotides (specifically AAX55180-771) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, including lung diseases, acthma, allergies, asthma, impeded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pulmonary vasoconstriction; inflammation; allergic rhinitis;
acute asthma; allergy; asthma; impeded respiration;
respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX53491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX53491 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUN-1998;
17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pulmonary hypertension; pulmonary vasoconstriction; emphysema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense oligonucleotide; multiple target; antisense treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                                                                                                                                           The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and
                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                               vasoconstriction
                                                                                                                                                                                                                                                                                           New antisense oligonucleotides used in
                                                                                                                                                                                                                                                                                                                               WPI; 1999-229400/19
                                                                                                                                                                                                                                                                                                                                                                                            (UYEC-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9913886-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           impaired respiration; inflammation; lung disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCACGCACGGCCGCCTGAGCCCG 1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATACCGCCACCTTCGAACACCCTACCGAGCGCGCCGCCGGCATCCATTCCGTGTACGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 37; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                              EAST CAROLINA
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respiratory distress syndrome, pain, cystic fibrosis,
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97US-0059160
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                                                                                                                                                                                                                                                                                              treatment of, e.g. pulmonary
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104376 CCCGGCCGGCGCCCCVGGCCVGCGGNNHNNNSGCCCGGCCGGCGCGCCCCVGGC
                                                                                                                                                                                                                                                                                                                                                          104613 CVGCGGNNHNNNSGGCGGCGCGCGCCCVGGCCVGGCGNNHNNNSCGGCGCGCGCGCCCVGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 114955 BP; 6071 A;
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                                                                                                                                                                                                                                                                                                              768 GCCGGTGGTGATCTCGCACCACAAGGTCATGGGCCAAGCCCAATTTCGGCCGCTCGCGCGA 827
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                                                                                                                                                                                                                                                                                                                                                                                                  AGGCGAGCACATCGTGGCCGCGCGGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGT 767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCGCGCCCVGGCCVGCGGNNHNNNSGCGCGCCCVGGCCVGCGGNNHNNNSGGCGCGCCCV 104672
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                                            CATCACCTGGTGCAAGCCCTTCCCCGAACTGAGCGGGCGCGACCTGGATGAAGTCGCGGC
                                                                                      CGCCCVGGCCVGCGGNNHNNNSC----CGGCCGGCGCGCCCCVGGCCCVGCGGNNHNNNS
                                                                                                                              GCCVGCGGNNHNNNSGGCCGGCGGCGCCCCVGGCCVGCGGNNHNNNSCGGCCGGCGGCG
                                                                                                                                                                                                                       GACGCTGCCGCTGATCGAGGCCGCCATGGCGCCCAGGACGTCTCGCTGGACGCGTATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 103; DB 20;
Pred. No. 4.2e-08;
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                                                                                                                                              Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1008
06-DEC-2001
                                                                                                  myasthenia gravis;
                                                                                                                                                                                                                                                            Human ORFX polynucleotide sequence SEQ ID NO:18057.
                                                                                                                                                                                                                                                                                                 24-JUN-2002
                                                                                                                                                                                                                                                                                                                                    ABN24790
                                                                                                                                                                                                                                                                                                                                                                 ABN24790 standard; cDNA;
                                WO200192523-A2
                                                                                                                                     mmune deficiency; immune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders; haemorrhage, osteoarthritis, neurodegenerative disorders disorders; related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 312 BP; 62 A; 92 C; 105 G; 52 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (referred to as open reading frame, ORFX, where X is 1-11491 (see in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human polypeptides and polynucleotides useful for diagnosing preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.B. The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
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29-AUG-2000;
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                            TCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACCGCGTG
                                                                                                                                                                                                                               TGGGTTGCGACTGCTATCCGTACACCGCAAGCTCGTCCACGCTGGACCTCAAGCAGGTG
                                                                        ATTGGGGCCGCGGGCGAGGTGCTGGAATCCATCGAAGGTGCACAGTGCTATCAGCCGG
                                                                                                                                                    TCGGCAAACATGCGCGCGTGCCGGTGGTGATCTCACACCTGAAATGCGCAGGCGCTGCCA
                                                                                                                                                                                        TCGGCCGCGAGCTGCACGTGCTGGTGATCTCGCACCACAAGGTCATGGGCCCAGCCCA
                                                                                                                                                                                                                                                                   CCACCCACATGCGCGACGAAGGCGAGCACATCGTGGCCGCGCTGGAGGAAACCTTCCGCA 748
                                                                                                                                                                                                                                                                                                         CGACCACCGAAGAAGTGATGGGCCTGGCGGAGCCGCTGGCCGAAGCTGGCGCGATCTACA
                                                                                                              ATTTCGGCCGCTCGCGCGAGACGCTGCCGCCTGATCGAGGCCGCCATGGCGCGCCAGGACG
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Pred. No. 1.
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; antibiotic; nysl; ds.
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/note= "CDS does not include
complement (1056..2576)
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/note= "CDS does not include
complement (62551..63615)
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product= "NysD1 protein"
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/note= "CDS does not include
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P-PSDB; AAE10125, AAE10126, AAE10127, AAAE10131, AAE10132, AAE10133, AAE10134,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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CCGCCCCCCGCGACCTGGCCGCCCTCGCCGACGCCGAAGGGCCCGTCCCCGACCTGGTCG
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s, Ellingsen
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ZOTCHEV S B.
SEKUROVA O N.
FJAERVIK E.
BRAUTASET T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65140 BP; 8270 A;
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TGACCCTGGAACAGGGCACCGCCCTCTTCGACGCGGCCCTGGCC
                                           AAGACCTGTCGCAGGCCAGCGGCATCGCGGTCTCGACCCTGTCC
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                                                                                                                                       AGGAAGTGATGGGCGCGCGCCTGCGCGCGCGAGCGCAAGGCCCCG---GAAAATGACCCTGC 1672
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               New nystatin polyketide synthase polynucleotides and polypeptides. useful as antibiotics and antifungals \boldsymbol{\cdot}
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10-APR-2000;
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Valla S, Ellingsen TE,
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ZOTCHEV S B.

SEKUROVA O N.

) FJAERVIK E.

) BRAUTASET T.
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complement (60238..61296)
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/product= "NysD2 complete
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Claim 1; Page 188-254; 266pp; English

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                                                        GCCTGATCCGCACCGCCACCGAGAACCCCGGCCGTTTCGCCCTCCTCGACCTCGCCC
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                                                                                    pseudorabies virus; PRV; LLV; large latency attenuated virus; vaccine; early protein 0; protecting animals; deletion mutants; swine;
                                                                                                                                                                                                                            AAQ73500 standard;
                                                                                                                                         DNA encoding Pseudorabies virus large latency transcript.
                                                                                                                                                                       15-MAY-1995
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                                                         Pseudorabies
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ73500 shows the Pseudorabies virus (PRV) large latency transcript (LLT). The basic sequence is derived from PRV strain InFh and PRV strain Ka. The LLT overlaps and is transcribed in the opposite orientation with respect to the EPO (early polypeptide 0) and the Immediately early gene (IE180). EPO is nonessential for replicatio, LLT is the only gene expressed during PRV latency, and the IE180 gene is absolutely necessary for PRV replication. However there are 2 copies of IE180 in the genome. It is expected that PRV lacking one of the IE180 copies is viable. Deletions in the non-overlapping regions of these 3 genes will generate single deletion routants, while deletions in overlapping regions will generate double deletion mutants.
                                                                                                                                                                                                                                                                                                                                                                                                                          mutants. The invention is concerned with the construction of attenuated viruses which have a reduced ability to reactivate from latency. This can be achieved by functionally disabling the expression of the EPO gene, or by disrupting the synthesis of the LLT, or both (See also AAQ73501 and AAR60620-24)
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                                                                                                                                                                                                                           5604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                              5544
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8438 BP; 1141 A; 2916 C; 3327 G; 1054 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New pseudorables virus mutants for use in vaccine - having a deletion and/or insertion in the early protein O gene or large latency transcript gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-1994.
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                                                            5484 TCCGCCTCCGCCACCTCCTCCTCCGCCGCGCCTCCGCCCCGGCCCCGGC---AGCCC 5428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Column 15-30; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USDA ) US SEC OF AGRIC.
211 GTCGCGCCCGGCTTCATCGACTCGCACACCACGACGACGACAACTACCTGCTCAGGCGTCGC
                                                                                                                                                                                                                                            CGCGCCGGGCCGCCACCGTCTCCGCCGGCCGCCCGCCGCCCCGCGCCCTCGGCCTCC 5485
                                                                                                                                                                                                                       TCCTCGTCCTCCTCCGAGGGAGAAGAAGACGAAGGAGTCCGGCCCGGCGCGCCCCACTCGCC 5545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1994-316187/39.
                                                                                                  GCCATCGGCGATCTGTCGGACGCCGCCGCGCACACCCCGGGTCGACGTGTCGGGCCTGGTG 210
                                                                                                                                                                                                                                                                                                         Conservative
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7014..8425
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/note= "RNA cap
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/note= "derived
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                                                                                                                                                                                                                                                                                                                         5.48;
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                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                       Score 94.2; DB 15
Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                      Mismatches 738;
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1344 4300	GGGCGCGGCAGCTGCAGGCCGGGTACTTCGCCGACCTGGTGGTGGTGTTCGACCCGGCCACG	1285 4359	Db dd
4360		4419	Db 42
) N		4474	Db -
1224	TELESTOCES TO THE TAY TO SEE THE TAY TO SEE TO SEE TO SEE TO SEE THE TAY TO SEE T	_ (Ογ
1164	GCGTTCGGCCCGACCATGATCGGCTCCGACGGCCTGCCGCACGACGACGACGCCCCGCATCCG	1105	g &
4528	GCGCTGCTCGCGACGCGATCCCCGGGGCCGGCCCGAGCGGCAGCAGCCGGCCG	4587	Db
1104	CTGCAGCCGGCCGCCATCTACTTCATGATGGACGAACCCGACGTGCAGCGCATCCTG	1045	Qy
1044 4588	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	985 4647	Qy Db
4648	GCCTGCGTCCTGGCGCGCGCGCGCTCCTCGAGCGCCTGCCT	4707	Db
984	GTGCTGCTGGCCGGACGCACCATCATCACCTGGTGCAAGCCCTTCCCCGAACTGAGCGGG	925	Qy
4708	GCGTCCGCCGCCGTCGCCGCCGCGCGCGTGCCCCGCGACCTGGCGGAC	4767	Db
924	GTCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACCGC	868	Qy
4768	TACCCGGGCCGCCCGGACCCCCGCGCGCGGGGAGGCCGACGA	4827	Db .
867	AATTTCGGCCGCTCGCGCGAGACGCTGCCGCTGATCGAGGCCGCCATGGCGCGCCAGGAC	808	δĀ
807 4828	GGCCGCGAGCTGGACGTGCCGGTGGTGATCTCGCACCACAAGGTCATGGGCCAGCCC	751 4887	Qy Db
4888	CAGGACCCGCTCTGGGCCCTGCCGCGCACGCGGTGAGCGCCGTGGCCATGAGCCGCCGCTAC	4947	Db
750	ACCCACATGCGCGAAGGCGAAGGCACATCGTGGCCGCGCGCG	691	Qy
4948	TCCTTCATCACCGGCAGGGTGACCCCGGCGCGCGCACATCGGGGACGGCATGGCCGCC	5007	Db
690	ACCACCGAAGAGATCATCGAGGTGTGCCGGCCGCTGAGCGCGCATGGCGGCATCTACGCC	631	Qy
5008	CCCGACCAGCGCTTCAACCAGTTCTGCCAGGGCGGGGTCCACGGGCCCACGGCCACGGC	5067	ф
630	ATGGCCAGCGGCGATCGGCATTTCGACCGGCGCCTTCTACCCGGCCGG	571	0γ.
5068	ATCTACAGCGGGGCCGAGGCCATGTCCTGGCTGCAGAACCCGCGGATGCAGGCC	5127	Db .
5128		211	0 5
10	CCGTCAACGCCGCTGTATGGTGGGCCATTCAACGCTGCGCGCGC		. Qy
5188		5247	Db
450	GGCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGGGCCACGCCGGCG	. 391	Qy
5248	GACCTCCGGCGACGGCGCTCCGCTACGGCGGCGACTCCCCCGGGACTCCCCCGAGGGGCTC	5307	Db
390		331	γQ
w	TCC -	0	Db -
ω		271	Qy
5368	GCCCGGCCCCGCGCAGGAAGCGCCGCCTCCACCAACAACCACCTCTCGCTCATGGCCGAC	5427	Db

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1345 GTGGCCGATACCGCCACCTTCGAACACCCTACCGAGCGCGCCGCCGG

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Query Match
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respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcolon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX53491 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4299 CCGGCGCCGGCGGCGCGCGCCCCTCCGGCCTCCCGGCTCCGG
                                                                                                                                                                                                                               non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pulmonary vasoconstriction; inflammation; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense oligonucleotide; multiple target;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-1999
                                                                                  inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize hepatic metastases, as well as all types of cancers which may metastasize
                                                                                                                                                                                                                                                                                                                                                                                              directed against at
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 37; 120pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense oligonucleotides used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYEC-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-1998;
17-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hepatocellular carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            impaired respiration;
                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                          specification describes antisense oligonucleotides (AAX52869-X55271) acted against at least 2 mRNAs selected from target genes, coding and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1999-229400/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adenosine
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                                     114955
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97US-0059160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Al receptor antisense oligonucleotide fragment.
                                     BP;
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                                     6071 A;
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   5.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kidney cancer; melanoma; hepatic metastasis;
                                   29417 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                       lungs,
   Score
                                                                       including
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   93.8;
                                     36712 G;
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   ВB
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   20;
                                     21328 T;
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                                       21427 other;
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NUNDINGGGCGCGCCGCCGGCCGGGCCGSNNNDNNGGCGCGCCGCCGGCCGGCCGSNNN 105253
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                                                        CGCCGGCCGGGCCGSNNNDNNCGCCGCCGGCCGGCCGGCCGGCCGGCCGGGCC
                                                                                            GTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACG
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1; Mismatches 880; Indels
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 16-AUG-2001
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/product= "NysD3 protein"
6338..27541
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/note= "CDS does not include
complement (1275..3092)
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complement (3070..4824)
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                                                                     'product= "NysI partial protein"
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ic; nys2; ds.
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14-APR-2000;
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(SNTF )
(ALPH-)
(SINV-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the cloning and sequencing of the cluster encoding a modular type Tolyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present sequence is a Streptomyces noursei nys2 DNA of nystatin PKS gene cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-2001;
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             CGTCAGGACGACGCGACCGGGCCTGGGCAGCCGACGTCGAGACCGCCCTGGGCACCACC
                                          GTCATGCCGGACTTGCAGCGCGCCGCCACCGACGAGGAAATCGCGGGCCATGCGGGACCTG
                                                                     ACCGCACCGCCGCCCTCACCGGCCGCTGGCTCGTGCTCGTCCCGCACGACCACCAGGAC
                                                                                    CAGACCGAACTGGACTCCTGGCGCTAC - - - CGCGTCACCTGGAAGCCGCGCGCGCGCGCCCC
                                                                                                                                          CTGGACGAAGGCGCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGG
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) ZOTCHEV S B.
) SEKUROVA O N.
) FJAERVIK E.
) BRAUTASET T.
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, Ellingsen TE,
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; 2000GB-0008786.
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letta H, Gulliksen O;
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The invention relates to an isolated ramoplanin biosynthetic pathway polypeptide selected from a polypeptide of open reading frames (ORF) 1-32. The isolated polypeptides are useful for chemically modifying a biological molecule that is a substrate for a polypeptide encoded by ramoplanin biosynthesis gene cluster, by contacting the biological
                                                                           Novel isolated ramoplanin biosynthetic pathway polypeptide chemically modifying biological molecule that is a substrat polypeptide encoded by a ramoplanin biosynthesis gene clust
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Location/Qualifiers complement (1321382) /*tag= a	omonospora c	Everninomicin; antibiotic; bottle-neck gene; orthomicin; fermentation; ds.	omonospora DNA e	AC AAS08693; XX	AAS08693 standard; DNA; 109519 BP.	7 11	TCGCCCGCTGGCTGCGCCACG	4/332 CHRIBACCHRACCHRACCHRACCHRACCHRACHCHRACHRACHRA	CCGATACCGCCACCTTCGAACACCCTACCGAGCGCCGCCGCCGCCATTCCGTGTACG	1289 GCGGGCAGCTGCAGGCCGGTACTTCGCCGACCTGGTGGTGTTTCGACCCGGCCACGGTGG 1348	TGGAGGCGGAGGAGAGCCGGCTCATGCTCGCCGCCGGTGAGGAGGCCGGCGCGGCCTGC	1199 TETROGECACCTICCCCCCCGCTCCTCCCCCCCACCTCCCCCCCCCC	TIGGCCGACGACGACGACGACGACGACGACGACGACGACGAC	AGCCGGCCGCGCCACTTACTTCATGATGGACCAACCCCACTGCCACCCAC	ACCTGGATGAAGTCGCGGCCGAGCGGCGAAATCCAAGTACGACCTGGTGCCCGAGCTGC	929 TGCTGGCCGGACGCACCATCATCACCTGGTGCAAGCCCTTCCCCGAACTGÂGCGGGCGCG 988	869 TCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACCGCGTGC 928	809 ATTTCGGCCGCTCGCGCGAGACGCTGCCGCTGATCGAGGCCGCCATGGCGCGCCAGGACG 868	749 TCGGCCGCAGCTGGACGTGCCGGTGATCGTCGCACCACAAGGTCATGGGCCAGCCCA 808	
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roduct "EvrI"

S85..30479

tag a h

roduct "EvrJ"

roduct a i

72..26676

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30557..31876)

CDS

RBS

product= "EvrH"
omplement (25230..25233)
*tag= af

plement (24177..25223) ag- ae ag- ac oduct- "EvrG" \$6..22740

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RESULT 12
AAZ87286
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                                                        Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma; chronic obstructive pulmonary disease; respiratory inflammation;

 venezuelae

                                                                                                                                                               05-JUN-2000
                                                                                                                                                                                                                        AAZ87286 standard; DNA; 1248
              Streptomyces
                                           hypercholesterolaemia;
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               venezuelae ATCC15439
                                                                                                                                                             (first entry)
                                                                                                                               desosamine biosynthetic gene desI,
                                           crop
                                          protection
                                           agent; ds
                                                                                                                                 SEQ ID NO:7.
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                                                                                                                                                                                                                                                                                                       CC biosynthetic gene cluster, or fragments thereof. The macrolide CC biosynthetic gene cluster encodes proteins which synthesise methymycin, permethymycin, narbomycin or a combination of these CC compounds. Recombinant or augmented cells comprising the desosamine CC and/or macrolide biosynthetic gene clusters are useful for the CC proteins are useful for synthesis of methymycin, pikromycin, cc neomethymycin and narbomycin. The alternative termination of polyketide CC polyhydroxyalkanoate (PHA) monomers. The compounds produced by the CC recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare CC immunosuppressants, agents to treat asthma, chronic obstructive pulmonary CC cholesterol-lowering agents or macrolide-based antibiotics which are cative against a variety of organisms, e.g., bacteria, including CC as viral parasitic pathogens, or as crop protection agents (e.g., CC fungicides or insecticides) via expression of polyketides in plants. CC sequences AA287286-287294 represent desosamine biosynthetic genes from CC CANATAIRS.
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Best Local S
Matches 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated and purified nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-1998;
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                                                                                                                                                                                                                                                                  Sequence 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces antibioticus. The invention also relates to a macrolide
                                                                                                                                                                                                                                                                                               Streptomyces venezuelae ATCC AAY77181-Y77189.
                                                                                                                                               215
 212
                                                                                                                   92
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 TCGCGCCCGGCTTCATCGACTCGCACACCCACGACGACAACTACCTGCTCAGGCGTCGCG
                              TCACCCCGGTCTTCGCCGACATCGACCCGGACACCGGCAACCTCGACCCGGACCAGGTGG
                                                         CCATCGGCGATCTGTCGGACGCCGCGCGCGCACACCCGGGTCGACGTGTCGGGCCTGGTGG
                                                                                      CCACCTGCAACGCCACGGCCGCGCCTCAGCTCCTCGCGACGCGACGCCGCCGCCTCACCGGCG
                                                                                                                                                                             2000-160679/14
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                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 353-354; 438pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e and macrolide biosynthetic of methymycin and pikromycin
                                                                                                                                                                                                          Conservative
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Pred. No. 0.
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                                   Glycosylated polyketide; modified recombinant bacterial host cell; mRBHC; macrolide; anthracycline; angucycline; avermectin; milbemycin; tetracycline; polyether; polyether; ansamycin; isochromanequinone; suga desosamine; DesI; 4-dehydrase; enzyme; gene; ds.
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            Streptomyces venezuelae
                                                                                                         Streptomyces venezuelae DesI gene
                                                                                                                                      23-SEP-2002
                                                                                                                                                                 AAD39044;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   for a particular metabolite via the recruitment and collaborative action of sugar genes from a variety of sugar blosynthetic pathways to yield a metabolite comprising a non-natural sugar, e.g., a novel glycosylated polyketide. The invention also relates to a modified recombinant bacterial host cell (mRBHC) in which the expression and activity of nucleic acids encoding sugar biosynthetic enzymes has been altered. The mRBHCs may be cultured to produce the modified sugar products, e.g. a macrolide, anthracycline, angucycline, avermectin, milbemycin, tetracycline, polyene, polyether, ansamycin or isochromanequinone. The present sequence is Streptomyces venezuale sugar (desosamine) biosynthetic gene cluster neer 1,4 debudges venezuale sugar (desosamine)
                                                                                                                                                                                                                                                                                                                                                                         Sequence 1248 BP; 177 A; 546 C; 377 G; 148 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified recombinant bacterial host cells in which the expression activity of nucleic acids encoding sugar biosynthetic enzymes has altered, useful for producing metabolites with altered sugar struc
                                                                                                                                                                                                                                                                                                                                                                                                            biosynthetic
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                                                                                         TCGCCCCCGCTTCATCGACTCGCACACCCACGACGACAACTACCTGCTCAGGCGTCGCG
                                                                                                                       TCACCCCGGTCTTCGCCGACATCGACCCCGGACACCGGCAACCTCGACCCGGACCAGGTGG
                                                                                                                                                    CCATCGGCGATCTGTCGGACGCCGCCGCGCACACCCGGGGTCGACGTGTCGGGCCTGGTGG
                     ACATGACGCCCAAGATCTCGCAGGGCCTCACCACGGTGGTCACGGGCAATTGCGGGCATCA 331
                                                                                                                                                                                                       ACGGCAGCAACACCCCGGGGCGCGCGCGACCTGGGCGTGCGCGGCGACCGCATCGCCG
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GCGCCGACCAGCTGCGGAAGGTCGCCGACGAGCACGGCCTGCGGCTGTACTTCGACG
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/transl_except= (pos:1..3, aa:Met)
/note= "CDS does not include start codon"
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Pred. No. 0.
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                                                                                                                                                                      Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromyc neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma; chronic obstructive pulmonary disease; respiratory inflammation;
                                                                                                                                                                                                                                                                                          05-JUN-2000
                                                                                                                                                                                                                                                                                                                                                         AAZ87284 standard; DNA; 12441 BP
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                                                                                                                            Streptomyces venezuelae ATCC15439
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                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                         desosamine biosynthetic gene cluster pikB,
98US-0105537
                              99WO-US14398
                                                                                                                                                          crop protection agent; ds.
                                                                                                                                                                                                                                                         SEQ ID NO: 3
                                                                                                                                                                                                                         pikromycin;
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Sequence 12441 BP; 1704 A; 4294 C; 4686 G; 1757 T; 0 other;

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useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary diseases as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                           compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, pikromycin, neomethymycin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desosamine and macrolide biosynthetic gene clusters, useful for, synthesis of methymycin and pikromycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-160679/14
P-PSDB; AAY77179.
                                           bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as croprotection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents the desosamine biosynthetic gene cluster from Streptomyces venezuelae ATCC 15439.
                                                                                                                                                                                                                                                                                                                                                                                are useful for synthesis of methymycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise me
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pikromycin, neomethymycin, narbomycin or a combination of these
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid segment
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Š 밁 δÃ 밁 Q 망 Ş В δδ γ 밁 Q Вр Matches Query Match 11982 32 92 Local Similarity CCACCTGCAACGCCACGCCGGGCTCCAGCTCCTCGCGCACGCCGCCGCCGCCTCACCGGCG CCATGTCCCAATCCGATTCCCAGCCCTTCGACCTGCTGCTCGCGGGGGGGCACCCTCATCG CCGCCGCGGTCACACCCCGCACCTCGGCCGTCGTCGGCGTCCACCTCTGGGGGCCGCCCCT 11743 TCACCCCGGTCTTCGCCGACATCGACCCGGGACACCGGCAACCTCGACCCGGACCAGGTGG CCATCGGCGATCTGTCGGACGCCGCCGCCACACCCCGGGTCGACGTGTCGGGCCTGGTGG ACGCCAGCAACACCCCGGGGGGGGGCGCGCGCGACCTGGGGCGTGCGCGGCGACCGCATCGCCG GCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGGGCCACGCCGGCGG GCCTGGCGCCGCCACGCCAACCCGCCCCCCCCCTGGACCTGCTGGACGAAGGCG GCGCCGCCGACCAGCTGCGGAAGGTCGCCGACGAGCACGGCCTGCGGCTGTACTTCGACG 11683 TCGCGCCCGGCTTCATCGACTCGCACACCCACGACGACACTACCTGCTCAGGCGTCGCG ACATGACGCCCAAGATCTCGCAGGGGGTCACCACGGTGGTCACGGGCAATTGCGGCATCA 331 Conservative 4.78; 0; Score 81.8; DB 21; Pred. No. 0.00011; Mismatches Length 12441; Indels 12; Gaps 11803 451 211 151 91 11863 11923 Ņ

AGGTCTTCAGCTTCCA----CGCCACCAAGGCCGTCAACGCCTTCGAGGGCGGCGGCCGTCG

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RESULT 15
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biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asth
chronic obstructive pulmonary disease; respiratory inflammation;
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                                                                                                                                                                                                                                                           biosynthesis; macrolide; polyketide; methymycin;
                                                                                                                                                                                 venezuelae ATCC15439.
                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                           /product= "PikB gene cluster
/note= "No initiation codon c
806..2014
/product- '6834..7402
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          protein
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pikromycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents,
                                                                                                                                                                                                                                                                                                                                                   biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster or fragments thereof, synthesise methymycin, biosynthetic gene cluster encodes proteins which synthesise methymycin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                 such as chemotherapeutics, immunosuppressants, agents to treat astima, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
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antibiotics
bacteria, in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Figure 32; 438pp;
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/note= "No termination codon given in the specifica
/transl_except= (pos:8270..8272, aa:Val)
/transl_except= (pos:8273..8275, aa:Thr)
/transl_except= (pos:8276..8278, aa:Gly)
/complement (10126..11139)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biosynthetic gene cluster (pik) from Streptomyces venezuelae ATCC 15439, as given in figure 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents the desosamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 CCATGTCCCAATCCGATTCCCAGCCCTTCGACCTGCTGCTCGCGGGGGGGCACCCTCATCG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                            GCCGCGAGCTGGACCTGCCGGTGGTGATCTCGCACCACAAGGTCATGGGCCAGCCCAATT
                                                                                                                                                                                                                                                                                                                ACGGCCTCAACAACCACCAGTACGTGATCGTCGAGGATCGACGAGGCCACCGGCATCC 11953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGGGGCCACGCCGGCGG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCTGGCGCCGCCGCCCCCCCTGGACCTGCACGAGGGCG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGCCGCCGACCAGCTGCGGAAGGTCGCCGACGAGCACGGCCTGCGGGCTGTACTTCGACG 12370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCATCGGCGATCTGTCGGACGCCGCCGCGCGCACACCCCGGGTCGACGTGTCGGGCCTGGTGG 211
  CCGAACGCCTCGCCGCGCGCGTGCTGTCCCTGCCGACCGGCACCGCCATCGGCGACGACG
                                                                                                     CCCACATGCGCGAAGGCGAGGAGCACATCGTGGCCGCGCTGGAGGAAAACCTTCCGCATCG 751
                                                                                                                                                                                                                                                                                                                                                                                                                      CCGCCTACCGCGAGCACCTCGCGGACCTCCCCGGCGTCCTCGTCGCCGACCACGACCGCC 12013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCACCGAAGAGATCATCGAGGTGTGCCGGCCGCTGAGCGCGCATGGCCGGCATCTACGCCA 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGGCCTCACCTCCGACGCGTTTCCCGAGGTCATCGACCGGAACCGGCGCAACCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCAGCGCGCCGCCACCGACGAGGAAATCGCGGCCCATGCGGGACCTGGCCGAGGAAGCCA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGCGCACGCCCTCGGCTGCGCGGTCGACGGCCGGCCGCCGCCGCCAGCCTCGGCGACGCCG 12310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGCGCCCGGCTTCATCGACTCGCACACCCACGACGACAACTACCTGCTCAGGCGTCGCG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCACCTGCAACGCCACGGCCGGGCTCCAGCTCCTCGCGCACGCCGCCGCCCTCACCGGCG 12610
                                                 AGGACGTCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACC 922
                                                                                                                                                            TCGGCCGCTCGCGAGACGCTGCCCGCTGATCGAG-------GCCGCCATGGCGCGCC 862
                                                                                                                                                                                                           ACCGCGACCTCGTCATGGAGGTCCTGAAGGCCGAAGGCGTGCACACCCCGCGCCTACTTCT 1189:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCCCGGCGGCAGCCCCGCCGGCGGGACCAACGCCAAGATGAGCGAGGCCGCCGCCGCCA 1213:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCACCGACGACGCCGACCTCGCCGGCCCGGGATCCGCGCCCTCCACAACTTCGGCTTCGACC 12193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACATGACGCCCAAGATCTCGCAGGGGCGTCACCACGGTGGTCACGGGCAATTGCGGCATCA 331
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ilarity 44.2%;
Conservative

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Pred. No. 0.00011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542;
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923 GCGTGCTGCCGGCCGGACGCACCATCATCACCTGGTGCAAGCCCTTCCCCGAACTGAGCG

- Db 11772 ACATCCGCCGGGTCGCCGACCTGCTGCGTCTCTGCGCGACCCGCGGCCGCGAACTGACCG 11713
- Search completed: January 14, 2003, 05:58:19
 Job time: 1874 secs

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GLLGRVVNPLGEPIDGKGPIQYTERRRVDVKAPGIIPRKSVHEPVQTGLKSIDTLIPV
GRGQRELIIGDRQTGKTAVAIDTILNQKAVNAGKDESAKLYCVIVAIGQKRSTVAQIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MDGRRCRAAPSEAARLITRAFRSRNQRGATERSLRPRSDGISPR
PRPPAPRRRGAVHPARRSGSWWRVPPRPCRQGRQRSRPRHSRRSARRARRPRLRPCRE
RIPVGRRGSCPWYSTSPVAGKEKEAAGGPAAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="CC3451"
6338. .6742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="madetkatdagqryaqslfeltiengslqkveadlkslkamvad
Sadlrrliaspafsaedkgkgltavakkagfqplttkflglvaangrtgdllgaisaf
Velsakhrgyvtaevvsaaalspaqlkgvqtalaqalgktpevstrvdpsllggkvr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5691. .6245)
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/gene="CC3450"
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GELAQYREMAAFAKFGSDLDASTQKMLARGERLTELLKQPQYAPLSVEEQVCVIYAGT
  GGHGDHAASVTPFWSRTG"
7951. .9258
                                                   /translation="mrfafsgiadlspdaarpgwnrralkpqdlvdpalglgvdgalf
DHALGAGVAAVLADPALDAVGGQHGSRTGGIGEGAHQGGHGRADEGGGHRPDRADPPF
AEDGLQTIDQKLAVRLLLHHPDHPEDGALDNRGQQHRQHHAQNTRSDKQSERCADDRE
                                                                                                                                                                                                                                                                                                                /gene="CC3453"
7328. .7864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="ATP synthase F1,
/protein_id="AAK25412.1"
/db_xref="GI:13425168"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGYLDGIPTSSVRRFEAEFLARLHSQHADLLEGIRTKKALDKDLENTLKSALDSFSST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTLEEHGALEYTTVVVASASEPAPLQYLAPFAGCAMGEWFRDNGLHGLIIYDDLSKQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(6831. .7283)
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/gene="CC3449"
                                                                                                                                                                                                                                                                                                                                                                                             apsraltaaackalakevgrvaafggetksldaedlarcnasakvaak"
                                                                                                                                                                                                                                                                                                                                                                                                                /translation~"MLSSDPKHRWGYRRRHPRGRAASTRISPILDLTATSPKPEGFLM
KLRSLAAVAALSVSMFAGSAFADGRIAAALDAPVAAKTKVVAGGAVFVCEGTECVSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="identified by match to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="CC3450"
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/db_xref="GI:13425167"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="ATP synthase
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                                                                                                                             /product="hypothetical protein"
/protein_id="AAK25415.1"
/db_xref="GI:13425171"
                                                                                                                                                                                                         transl_table=11
                                                                                                                                                                                                                                 codon_start-1
                                                                                                                                                                                                                                                          note="identified"
                                                                                                                                                                                                                                                                                     /gene="CC3453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
/protein_id="AAK25414.1"
/db_xref="GI:13425170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="CC3452"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product="hypothetical protein"
'protein_id="AAK25413.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="CC3451"
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                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14432 ACACCCACTATGACGGCCAGGCGACCTGGAGCGGTCAGCTTGGCCCCAGCTCCGGCCACG 14373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 CCGACTACCTGGACGCGTTGCGGG 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 ACCCGCCCGCCCCCTGGACCTGCTGGACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
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Sequence 1 from Patent WO0159126.
AX211705
                                                                                                                                                                                                      Gene cluster encoding a nystatin polyketide synthase and manipulation and utility Patent: WO 0159126-A 1 16-AUG-2001;
                                                                                                                                                                                                                                                                              1 (bases 1 to 65140)

Zotchev,S.B., Sekurova,O.N., Fjaervik,E., Brautaset,T. Stroem,A.R., Valla,S., Ellingsen,T.E., Sletta,H.V. and
                                                                                                                                                                                                                                                                                                                                                                           Streptomyces nourse
                                                                                                                         Norges Teknisk Naturvitenskapelige Universitet (NO); STIFTELSEN IND OG TEKNISK FORSKNING VED NORGES TEKNISKE HOOSKOLE (NO); IND OG TEKNISK FORSKNING VED NORGES TEKNISKE HOOSKOLE (NO); ALPHARMA AS (NO); Sinvent AS (NO); Zotchev, Sergey Borisovich (NO); Sekurova, Olga Nikolayivna (NO); Fjaerrik, Espen (NO);
                                                                                                                                                                                                                                                                  Gulliksen, O.M.
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                                                                                                             Brautaset,
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/product="acyl-CoA dehydrogenase
/protein_id="AAK25416.1"
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/organism="Streptomyces noursei"
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                                             CCGACACCGGCCGGACCCCGAGACCCTGGC-----CACCGCCCTGGCCGCCAGCC
                                                                                                                       CCACCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCATCATCACCTGGTGCA 961
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                                                          AGCCCTTCCCCGAACTGAGCGGGCGCGACCTGGATGAAGTCGCGGCCGAGCGGGCAAAT 1021
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                                                                                     1616 AGGAAGTGATGGGCGCGCGCCCTGCGCCGAGGCCCCG---GAAAATGACCCTGC
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TGACCCTGGAACAGGGCACCGCCCTCTTCGACGCGGCCCTGGCC
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Search completed: January 14, Job time : 5425 secs 2003, 08:07:30